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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                       protein search, using sw model
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Run on:

August 9, 2004, 16:39:47; Search time 48 Seconds (without alignments) 3025.613 Million cell updates/sec

US-09-987-701-2 Title: Perfect score:

514 1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

1586107 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* 1: geneseqp1980s:* South Works

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* 2: geneseqp1990s:* 3: geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMMITES

N	ion	Aab95225 Human pro	7190	Human	00	4	Abg21351 Novel hum	9		Novel	Abr52980 Protein s	21	Abb59486 Drosophil	~	Abb62260 Drosophil	Aab68284 Amino aci		Aab92844 Human pro			Aar85881 WD-40 dom	Aag14893 Arabidops	119	5040	Aab68282 Amino aci	Aag48120 Arabidons
SUMMAKIES	Ð	AAB95225	19	ADD14051	ABP41760	ABP51424	ABG21351	ABB60376	AA004385	ABG21350	ABR52980	ADA13321	ABB59486	AAY79678	ABB62260	AAB68284	AAB68516	AAB92844	ABB97306	ABR53774	AAR85881	AAG14893	AAG48119	04	AAB68282	AAG48120
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AAG14894 AAW55957 AAW58988 ADE59633 ADE59705 ADE59709 ADE83378 ADE59701 ADE59713 ADE59713 ADE59713 ADE597145 AAM93784 ABB99407	ABB10141 ABP66728 ADE54235 AAR70002 ADE58488
	40101
	521 521 409 409
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	348 346.5 344.5
	4 4 4 4 4 1 5 6 4 6

ALIGNMENTS

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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                       Human protein sequence SEQ ID NO:17352.
             AAB95225 standard; protein; 514 AA
                                                                                                                                               27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAX-2000; 2000JP-002183767.
99-JUN-2000; 2000JP-002418997.
                                                                                                                          28-JUL-2000; 2000EP-00116126.
                                                                                                                                         99JP-00248036.
                                         (first entry)
                                                                                                                                                                                 (HELI-) HELIX RES INST
                                                                                                                                         29-JUL-1999;
                                                                                   Homo sapiens.
                                                                                               EP1074617-A2.
                                         26-JUN-2001
                                                                                                             07-FEB-2001.
                            AAB95225;
RESULT 1
AAB95225
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Saito K, , Otsuki Hayashi K, S A, Nagai K, Isogai T, Nishikawa T, Sugiyama T, Wakamatsu Ota T, Is Ishii S,

Yamamoto J; T;

WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 8; SEQ ID NO 17352; 2537pp + Sequence Listing; English

The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

03-JUN-2002; 2002WO-US017382.

WO200299122-A1. Homo sapiens.

12-DEC-2002

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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises at least is nucleotides and the combination of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13633 to AAH13642 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
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Matches 511;
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The invention relates to identifying (MI) a candidate p51 pathway in modulating agent, by contacting an assay system comprising a purified HW modulating agent, by contacting an assay system comprising a purified HW polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but correctly and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising or contacting a cell defective in p53 pathway of a cell (comprising or that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restorately, modulating and mammalian cell (Comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising the sample with a probe for HM corresponding to a patient (comprising the sample with a probe for HM expression, (c) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful correctly in a patient, where the cancer has greater than 25 * expression cancer, and patient cancer has greater than 25 * expression lead to the p53 pathway. Such as, angiogenesis is related therapeutic applications, where disease or disorder prognosis is related therapeutic applications, where disease or disorder prognosis is related therapeutic applications, where disease or disorder prognosis is related therapeutic applications, where disease or disorder prognosis is related therapeutic and profile and the cell, so that the cell undergoes normal control feration of the cell, so that the cell undergoes normal control feration of the cell, so that the cell cycle (M2) and (M3) are useful for treating defects in the p53 pathway such as angiogenic, contacting the present sequence contacting the cell in the p53 pathway such as angiogenic, contacting the cell in the cell cycle also the cell for modulating def
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                                                                                                                                                                                                                                                                                                                     Funke RP;
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Local Similarity 99.4%; Pred. No. 2.2e-242;
Hes 511; Conservative 1; Mismath.
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                                                                                                                                                                            05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                                                                                                                                                                                                        Friedman L, Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathway in Drosophila.
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Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

Human p53 modifying protein, SEQ ID 150.

13-AUG-2003 (first entry)

ABO07190 standard; protein; 514 AA

RESULT

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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of cells, determining whether the cells express a plurality of markers, and correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels
                                                          300
                                                                                                                    360
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                                                                                                                                                                                                                                                           GNILLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF 420
                                                                                                                                                                                                                                          480
                                                                             ATGSYDGFARIWTXDGNLASTLGQHKGPIFALKWNKKQNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                        KQQFPFKSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                                                                    KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                                                                                                                                                                                          DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSY
                         SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                          ATGSYDGFARIWTKDGNLASTLGQHKGP1FALKWNKKGNF1LSAGVDKTT11WDAHTGEA
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SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein
                                                                                                                                                                                                                                                                                                      514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human src biomarker polypeptide SEQ ID NO:240.
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Б
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                                                                                                                                                                                                                                                                                                                                                                                                              ADD14051 standard; protein; 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polymuclectides and polypeptides that predict compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polymuclectides or polypeptides, and selecting polymuclectides or polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of the microarray. The polymuclectides and polypeptides have cytostatic activities, and can be used in gene therapy. The polymuclectides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized cancer; based on patient aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present cancer invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 BAEVSINEDGTLFDGRFIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAA--- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 VTSLDWNTNGTILATGSYDGPARIWTEDGNLASTLGQHKGPIFALKWNRKGNYILSAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 MSITSDEVNFLYYRYLQESGFSHSAFTFGIESHISQSNINGTLVPPAALISILQKGLQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 EAEISINEDGTVFDGRPIESLSLIDAVMPDVVQTRQQAFREKLAQQQASAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 ATAATTTSAGVSHQNPSKNREATVNGEBNRAHSV-NNHAKPMEIDGEVEIPSSKATVLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 VISLDWNSEGTLLATGSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 KTTIIWDAHTGEAKQQFPFHSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 HINEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 HTNEVNAIKWDPSGMLLASCSDDWTLKIWSMKQEVCIHDLQAHNKEIYTIKWSPTGPATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 ------ASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRG
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tumour; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                          tch 89.4%; Score 2437; DB 7; Length 577; al Similarity 86.0%; Pred. No. 4e-217; 453; Conservative 33; Mismatches 27; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 IWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
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cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian antigen HNOKM38,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          Sequence 577 AA;
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155 186 214

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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
infertility; pregnancy disorder, anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorthoea; endocrine disorder; infection; infinamatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cycostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.8%; Score 2340; DB 5;
85.4%; Pred. No. 3.8e-208;
ive 32; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 2892; 2922pp; English.
                                                                                                                                                                                                                              SCI INC.
                                                                                                                                                                                07-JUN-2001; 2001WO-US018569
                                                                                                                                                                                                      07-JUN-2000; 2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.43
Matches 434; Conservative
                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                      CE, Rosen CA;
                                                                                                                                                                                                                                                                             2002-147878/19.
                                                                                                                                                                                                                                                                                         N-PSDB; ABQ54837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 542 AA;
                                                                                                                                  WO200200677-A1.
                                                                                                            Homo sapiens.
                                                                                                                                                         03-JAN-2002.
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The invention relates to 2175 novel human ovarian antigens (ABB41054-ABB43228) and to cDNAs encoding them (ABG54131-ABG56305), and also encompasses polypeptides 90% identical and polybrucleorides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen corrections and host cells comprising human ovarian antigen and the use of ovarian antigens, and the use of ovarian polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tunnours of ovarian or breast origin, reproductive system disorders (e.g., infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxinc shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired chockers) inflammatory conditions (e.g., mastitis, oophoritis and inflammatory disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders, neurological disorders, gastrointestinal disorders and urinary system disorders, ovarian antigen polypeptides and of polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may also be used in forensic analysis, and the collection of individuals and in forensic analysis, and the collection of individuals and in forensic analysis, and the sequence data for this parent did netering and phenotyphing. The polymucle of sequence data for this parent did netering and them parent of the printed control of the invention. Note: The sequence data for this parent did netering antigen of the invention. Note: The sequence data for this parent did netering antigen polymore of the printed of sequence data for this parent did netering and the
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28; Indels

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CSDDMTLKIWSWKQEVCIHDLQAHNKEIYTIKWSPTGPATSNPNSNIMLASASFDSTVRL 454
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GFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                                                                                                             HSAPALDVDWQNNTTFASCSTDWCIHVCRLGCDRPVKTFQGHTNEVNAIKWDPSGWLLAS
                                                                                                               156 REATVNGEENRAHSV-NNHAKFWEIDGEVEIPSSKATVLRGHESEVFICAWNPVSDLLAS
                                                                                                GSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLLATGSYD
                                                                                                                                                                       275 GFARIWIEDGNLASTLGQHKGPIFALKWNRKGNYILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                                                                                                                                                                                                                               GENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLAS
                                                                                                                                                                                                               HSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                                                               WDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGI
                                                                                                                                                                                                                                                                      CSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRL
                                                                                                                                                                                                                                                                                                                                                                                       487 FEVCWNAAGDKVGASASDGSVCVLDLRK 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP51424 standard; protein; 395 AA.
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05-SEP-2000; 2000US-0229751P
06-SEP-2000; 2000US-02305051P
06-SEP-2000; 2000US-02305059
06-SEP-2000; 2000US-0230518P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MDDT SEQ ID NO 446.
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05-SEP-2000; 2
05-SEP-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Gaps
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The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a treatment (MDDT) polypeptide (I) selected from a polypeptide having a treatment (MDDT) polypeptide (I) a beloted from the sequence selected from 254 sequences (BABP121.ABP1484) given in the specification, a naturally occurring polypeptide comprising a sequence (I) a beful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hypridoma technology.

CC preparing a polyclonal or monoclonal antibody by hypridoma technology.

Nucleic acids (II) (AB972449-AB9720) encoding (I) are useful for screening a compound for effectiveness in altering expression of a target of polymucleotides and antibody by hypridoma technology.

CC Screening a compound for effectiveness in altering expression of a test compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a bample, for detecting (I) in a sample, or for detecting (I) in a sample, and for purifying (I) from a sample. A composition comprising (I), an associated with decreased or increased expression of functional MDDT. Or (II) are useful for diagnosing, treating or preventing disorders are selected from a cell proliferative disorder such as arteriosclerosis, or (II) are useful for diagnosing, treating or preventing disorders are selected from a cell proliferative disorder and an autoimmune/inflammatory disorder such as AIDS, Addison's disease, all automatory disorder such as AIDS, Addison's disease, and automatory disorder such as AIDS, Addison's disease or chemisted or transgenic animals to model human disease; in somatic or theumatoric arimals to medel human disease; in somatic or type, for detecting differences in the chromosomal location due to companiences.

CC deminnes
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                                                                                                                                                                                                                                                                                         Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS;
Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE;
Dahl CR, Momiyama MG, Bradley DL, Rohatqi SD, Harris B;
Roseberry AM, Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V;
Daffo A, Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578; 618pp; English.
06-SEP-2000; 2000US-0230598P.
06-SEP-2000; 2000US-0230599P.
06-SEP-2000; 2000US-0230865P.
06-SEP-2000; 2000US-0230988P.
06-SEP-2000; 2000US-0230988P.
07-SEP-2000; 2000US-0230989P.
07-SEP-2000; 2000US-023098P.
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                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
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Matches 389; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Page
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                                                                                                                                                                                                           301 KOOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 360
                                                                                          SDLLASGSGDSTARIWNLSENSTSGSTQLVLKHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                            245 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAMNPV
                                125 OGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICANNPV
                                                                   SDILLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                         241 ATGSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                          GNLLASCSDDMTLKIWSMKQDNCVHDLQAHN 395
                                                                                                                                                                                                                                                                                   GNILLASCSDDMTLKIWSMKQDNCVHDLQQHN 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #21342.
                                                                                                                                                                                                                                                                                                                                                                                                          ABG21351 standard; protein; 584
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23-AUG-2000; 2000US-00649167.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS737-ABB2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                              solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                        ID NO 7920; 21pp + Sequence Listing; English
                                                                                                                            Myers EW;
                                                                                                                             PWD,
                                                      2000US-0191637P.
2000US-00614150.
                            23-MAR-2001; 2001WO-US009231.
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11-JUL-2000;
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Matches 385;
 27-SEP-2001
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                                                                                                                                                                                                                                                                          --- AAASQQGSA 124
                                                                                                                                                                                                                                                                                            diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent din not appear in the printed specification, but was obtained in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                              ASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKDVTSLDWNSDGTLLANGS
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                                                                                                                                                                                       Indels
                                                                                                                                                          70.0%; Score 1907.5; DB 4;
llarity 65.1%; Pred. No. 6.7e-168;
Conservative 34; Mismatches 36; 1
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Best Local Similarity
Matches 371; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                   61 EVEWSYGEDGEV--ARPIEGLSLIDAVMPEVKPLKPIVKTEFGKPGAVDSSAPAGGNQNN
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                     Gaps
 Length 700;
                     Indels
DB 4;
69.9%; Score 1904.5; DB 4 54.8%; Pred. No. 1.7e-167; ive 51; Mismatches 75;
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signalling, insecticide;

Drosophila melanogaster polypeptide SEQ ID NO 7920

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ABB60376 standard; protein; 700

developmental biology; cell

Drosophila melanogaster.

pharmaceutical

WO200171042-A2

1 HCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFAL 60

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NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNAN 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynuclectides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to evytokine, cell proliferentiation or which may induce production of other cytchines in other cell populations. The production of other cytchines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytchine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                  Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                                                                                                          TGALVHSYRGIGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                             AA004385 standard; protein; 208 AA
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18-MAY-2000; 2000US-00577409.
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Matches 206; Conservative
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N-PSDB; AAI84316.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics of disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABGOO10-ABG30377 represent novel human diagnostic manno acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                        121 VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNK 180
                                                                                           333 VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNK 392
KWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIH 332
                                            61 KWNKKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping; gene mapping; gene therapy, forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 51709; 103pp; English.
                                                                                                                                                                                    393 EIYTIKWSPTGPGTNNPNANLMLASAS 419
                                                                                                                                                                                                                 EIYTIKWSPTGPGTNNPNANLMLASAS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #21341.
                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                 ABG21350 standard; protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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N-PSDB; AAS85537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
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273
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97;

Length Indels 49 20

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155 219 214 279 274 324 334 384 394 444 444 481

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us-09-987-701-2.rag

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50 ISIIQKGLQYVEABVSINEDG---TLFDGRPIBSLSLIDAVMPDVVQTRQQAYRDKLAQQ 106
                                                                                                                                                                                                                                                                                                          .07 QAAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 IFAGRISQDGQKYAVAFMDGQVNVYDLKKLNSKSRSLYGNRDGILNPLPIPLYASYQSSQ 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                215 SSGKTINQVFCLAMSHDGNSIVTGVENGELELMNKTGALLNVLNFHRAPIVSVKMNKDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 FILSAGVDKTTIIWDAHTGEAKQQFPF------HSAP---ALDVDWQSNNTFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 CSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 PGPKGAIFVYQITEKTPIGKLIGHHGPISVLEFNDINKLLLSASDDGTLRIWHGGNGNSQ
                                                                                                                                                                                                                                         51 VNLVQRGILYTESELMVDSKGDISALNEHHLSEDFNLVQALQID-------KEKFPEI
                                                                                                                                                                                                                                                                                                                                          167 GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTQ-----LVLRHCIREGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 HIISMDVENVTILWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 HDLQQHNKEIYTIKWSPTGPGTNNPNANLMLAŞAŞFDSTVRLWDVDRGICIHTLTKHQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 NCFYGHSQSIVSASWV-----GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 ODVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGOHKGPIFALKWNKKGN
                                                                                                        -----FTFGIKSHISQSNINGALVPPAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, intracellular signalling molecule; INTSIG; cell proliferative disorder; cancer; atherosclerosis; autoimmune disorder; inflammatory disorder; infection; neurological disorder; developmental disorder; endocrine disorder; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; cerebroprotective; immunosuppressive; antiinflammatory; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human intracellular signalling molecule INTSIG-3, SEQ ID
                                                                                                                                   Query Match
18.3%; Score 499.5; DB 6;
Best Local Similarity 24.9%; Pred. No. 4.3e-37;
Matches. 142; Conservative 100; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 VYSVAFSPDGRYLASGSFDKCVHIW----NTOTGAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 GTGGIFEVCWNAAGDKVGA--SASDGSVCVL 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 DNDYIFDLSWNCAGNKISVAYSLQEGSVVAI 535
                                                                                                        1 MSISSDEVNFLVYRYLQESGFSHSA-
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                                                                                                                                                                                                                                                                                                                                                  RIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                                                    369
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                                                                                                                                                                                                                                                    RIWTENGNLAITLCQHKGPIFALKWNKKGNYVLSAGVDKTTIIWDAHTGEAKQQFPFHSA
                                                                                                                                                                                                                                                                                                                    PALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSD
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                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMTLKIWSWKQEVCIHDLQAHNKEIYTIKWSPTGPATSNPNSNIMLA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 825; 17pp + Sequence Listing; English
                                                                                                                   Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                          DMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLA
                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multiprotein complex; eukaryote; drug target; diagnosis
                                                                                                                                                                   10;
                                                                                                              ; Score 819; DB 4;
; Pred. No. 1.4e-67;
13; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i P, Krause R, K
Superti-Furga GD;
                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 535
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                                                                                                                30.0%;
86.2%;
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Marzioch M, Schultz JD,
                                                                                                                                                                      Matches 144; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein sequence #SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLZOME AG
                                                                                                                                              Similarity
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                                                                     Sequence 167 AA;
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                                                                                                                Query Match
Best Local
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NO:3

2001US-0313245P. 2001US-0314751P. 2001US-0316752P.

17-AUG-2001; 2 24-AUG-2001; 2 31-AUG-2001; 2

Sequence 535 AA

16-AUG-2002; 2002WO-US026322.

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Drosophila; der
pharmaceutical
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                                  360
                                                                                          313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 45 human intracellular signalling molecules (INTSIG), INTSIG-1 to INTSIG-45, and the cDNAs encoding them (ADA1319-ADA1408). The invention also encompasses expression constructs, host calls and transgenic organisms comprising an INTSIG nucleic acid sequence; the recombinant preparation of a INTSIG, an antibody against a INTSIG; methods of detection of INTSIG proteins or nucleic acids; am micro-array containing INTSIG nucleic acids; methods of screening compounds for their ability to modulate INTSIG acitvity or expression; and pharmaceutical compositions comprising an INTSIG protein, an INTSIG antibody, an INTSIG aponist or INTSIG antagonist. The INTSIG proteins, mucleic acids or compositions comprising them are useful in diagnosing, treating or compositions comprising them are useful in diagnosing, treating or preventing a variety of disorders, including cell proliferative disorders (e.g., AIDS, allergies, anaemia, asthma, Dronchitis, gout, multiple sclerosis, osteoarthritis, rheumatoid arthritis, or systemic lupus cervhemanosus; neurological disorders (e.g., epilepsy, stroke, alloredres disease); viral, bacterial, fungal, parasitic, protozoan or helminthic infections; neurological disorders (e.g., epilepsy, stroke, Alzheimer's disease); developmental disorders (e.g., achondroplastic disorders (e.g., disorders of the hypothalamus or pituitary gland or disorders (e.g., disorders of the hypothalamus or pituitary gland or disorders (e.g., cypletic fibrosis or hypercholesterolaemia). The present sequence represents an INTSIG protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPDKTCKLWSVETGK------CYHTFR-----GHTAEIVCLSFNPQSTLVATGSMDT 199
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                                                                                                                                                                                                                                                              Emerling BM;
cha SD, Lee EA;
1 BM, Gietzen KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                 Nguyen DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human intracellular signaling molecules (INTSIG)), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant INTSIG expression e.g. cancer, diabetes, epilepsy, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 CAEISSASFNW-----DCSLILTGSMDKTCKLWDATNGKCVATLTGHDDEILDSCFDY
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                                                                                                                                                                                                                                                                                                                                                                              L, L, Tran V
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                                                                                                                                                                                          JU DAM, Swarnakar A, Tang YT, Grillin, Becha S., IJ, Yao MG, Ramkumar J, Richardson TW, Becha S., A, Lehr-Mason PM, Baughn MR, Li JX, Duggan BM, Gi, Lehr-Mason PM, Baughn MR, Li JX, Vu Y, Lee S, S., Wi, Ison CH, Thangavelu K, Xu Y, Lee S, Y, Hafalia AJA, Ding L, P., Thangavelu K, Yu Y, Lee S, Thangavelu K, Yu Y, Lee S, Thangavelu K, Yu Y, The S, Thangavelu M, Yu Y, The S, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 414;
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; Pred. No. 1.2e-25;
49; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 225-226; 367pp; English
                     14-SEP-2001; 2001US-0322188P.
28-SEP-2001; 2001US-032330P.
12-OCT-2001; 2001US-032852P.
12-OCT-2001; 2001US-034568P.
12-APR-2002; 2002US-0372499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%;
28.3%;
   2001US-0316847P
                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.7
Best Local Similarity 28.3
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTASGEELN---
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N-PSDB; ADA13366.
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                                                                                                                                                                                                                                                                                                                                                  Lal PG, Borow
Elliott VS, S
Honchell CD,
31-AUG-2001;
                                                                                                                                                                                                                                                                                                                                   er.
PG,
-t VS,
CD
                                                                                                                                                                                                                                                                                             Forsythe Id
Warren BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections.
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419
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                                                   ---NPOGNHLLTGSS 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016-ABL10511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB7072). The sequence data for this parent aid not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --EGGOD-----VPSNKDVTSLDW-----NSEGTLLATGSYDGFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 KNEBATPYLFFVGEDEIKKSLEDT-LDLASVDTENVIDIVYQPQAVFKVRPVTRCTSSMP
TGN1LASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 GHESEVFICAWNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                             469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 481;
                                                                                                             FDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIW
                                                                                                                                            125 KNGENTAN----GEENGAHTIANNHTDMMEVDG----DVEIPPNKAVVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 5250; 21pp + Sequence Listing;
                                                TGKLIATASADGTARÍFSAATRKCIAKLEGHEGEISKISF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 5250.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EW;
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                                                                                                                                                                                                                                                                                                             ABB59486 standard; protein; 481
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
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Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL03589
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18; 192 133 221

Gaps

90;

Indels

275 251 335 298 382 357 442 408 501 468

191

---EGGOD----

us-09-987-701-2.rag

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signalling process in both Drosophila and Xenopus embryos. The Notchless protein has a novel highly conserved N-terminal domain followed by 9 WD40 repeats. Notchless, and nucleic acids enceding it, can be used in methods for the diagnosis and therapy of certain diseases, particularly cancer and neurodegenerative diseases (Claimed). A Notchless mutant in a sensitised Notch genetic background is used in a claimed method for identifying compounds capable of modifying the levels of expression or activity of a Notch protein
                                                                                                                                                                                                                                                                                                                                                               192 SGHKKHINCLAWEPYHRDPECRKLASASGDGDCRIWDVKLGQCLMNIAGHTNAVTAVFWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 LGQDRPIK-TFQGH----TNEV----NAIKWDPTGNLLASCSDDMTLKIWSMKQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 TGPFHPVKDRSKSHLSLSTBELQESALKRYQAVCPDEVBSLV-SCSDDNTLYLWRNNQNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 CVERMIGHONVVNDVKYSPDVK-----LIASASFDKSVRLWRASDGQYMAIFRGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 VRLWDLNTETPHFTCTGHKQWVL--CVSWAPDGKRLASGCKAGSIIIWDPETGQQKGRPL
                                                                                                                                                                                                                                                                                                                                              222 VPSNKDVTSLDW-----NSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWN
                                                                                                                                                                                                                                                                                                                                                                                                   276 KKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCK
                                                                                                                                                                                                                                                                                                                                                                                                                             252 GAG-LIYTSSKDRTVKNWRAADGILCRTFSGHA-----HWVNN---IALSTD---YVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 EPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGAS
                                                                                                                                                                                                                                 147 DMMEVDG----DVEIPPNKAVVLR------GHESEVFICAMNPVSDLLASGSGDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                             DB 3; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 13572
                                                                                                                                                                             Query Match
13.6%; Score 370; DB 3; L
Best Local Similarity 28.4%; Pred. No. 4e-25;
Matches 120; Conservative 55; Mismatches 158;
                                                                                                                                                                                                                                                                                         193 ARIWNLSEN----STSGSTQLVLRHCIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 411
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504
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                                                                                                                                                    Sequence 479 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383
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                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of Notchless, a novel protein of Drosophila. Notchless was identified in a screen for dominant modifiers of a Notch mutant phenotype in the Drosophila wing. The mutant dominantly suppressed the wing notching phenotype of notchind mutations, and the Notchless protein was shown to bind to the cytoplasmic domain of Notch. Notchless
                                                                                                                                                                                                                       476
                                                                                                                                                                  416
                                                                                                                                                                                                                                       PALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIK-TFQGH----TNEV-----NAIK 356
                                                                                                                                 384
                                                      IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 has
             PDEVESLV-SCSDDNTLYLWRNNONKCVERMTGHONVVNDVKYSPDVK-----LIA
                                                                       WDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLA
                                                                                                                                                                                                                       SASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "sequence deduced from nucleotide sequence additional Lys residue between Lys-67 and Ser-68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel notchless protein and nucleic acids encoding them useful treating and preventing cancer and neurodegenerative diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notchless, Nle gene, Notch, signalling, neurodegenerati
cancer, diagnosis, cytostatic, neuroprotective, therapy
                                                                                                                                                                                                                                                                                                     AQELPGHADEVFGVDWAPDGSRVASGGKD 473
                                                                                                                                                                                                                                                                               VHSYRG-TGGIFEVCWNAAGDKVGASASD 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "encoded by CAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27. .105
/note= "Nle domain"
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                                                                                                                                                                                                                                                                                                                                                                              AAY79678 standard; protein; 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EUMO-) EURO MOLECULAR BIOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila Notchless protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98GB-00024045.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                               invention is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLATGSYDGFARIW--TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGBAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------YC----VKTYTGHREWVRMVR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 WDFTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP-----TGPGTNN 408
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                                                                                                                                                                                                                                                                                                                      6 DEVNFLVYRYLQESGFSHSAFTFGIKSHIS---QSNINGALVPPAALISIIQKGLQYVEA 62
                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in alucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA sequences (ABL16176-ABL10511), expressed DNA ABR2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                     -----QDVA-----FDAQGK
                                                                                                                                                                                                                                                                                                                                                                                                           123 SAKNGENTANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSD
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                            13.5%; Score 368; DB 4; Length 411; 22.7%; Pred. No. 4.8e-25; ive 76; Mismatches 151; Indels 148;
                                                                                                                 Disclosure; SEQ ID NO 13572; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 LMVSASEDATIRIWDFETGEYERSLKGHTDSV-
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                     EM.
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standard; protein; 485 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220
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                                                                                                                                                               bone marrow transplantation; rheumatoid arthritis; lupus erythematosis; multiple sclerosis; encephalitis; vasculitis; diabetes mellitus; pancreatitis; gastritis; thyroiditis; malignant disorder; asthma; lepramatosis; gastritis; skin tumour; adrenal tumour; lung tumour; wound healing; growth disorder; inflammatory disease; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTILIWDAHTGEAKQQFPFH-- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- QSNNTFASCS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotide encoding TZap protein involved in T cell activation, useful for diagnosing and treating diseases involving T cell activation, for treating organ transplantation rejection, rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "unspecified residue encoded by
                                                                                                                                      transplant
                                                                 acid sequence of a human TZap gene cDNA clone.
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                                                                                                                                      T cell activation; immune response;
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inflammatory and/or infectious diseases
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25-FEB-2000; 2000US-0185016P.
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(first entry)
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⁴⁴⁶ YSVAFSPDGRYLASGSFDKCVHIW 469 |:| :||||:||| 460 YAVDWSPDGQRVASGGKDKCLRIW 483

Search completed: August 9, 2004, 16:45:24 Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

August 9, 2004, 16:40:42; Search time 8.66667 Seconds (without alignments) 3088.161 Million cell updates/sec

US-09-987-701-2 2726 1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 Total number of hits satisfying chosen parameters:

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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20	339.5	12	33		WDR5_HUMAN	
21	339	12	80	7	T2D4_HUMAN	homo
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23	329	12	79	Н	T2D4 YEAST	
24	321	11	37	Н	YKY4_CAEEL	
25	319.5	11	9	Н	PF20 CHLRE	
56	317.5	11	57	Н	SE10 CAEEL	
27	310.5	11	70	Н	T2D4_DROME	_
28	309	11	119	Н	Y143_SYNY3	
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T2D4 SCHPO TU11_SCHPO YLLL_CABEL GBB5_HUMAN GBB5_MOUSE FU12_SCHPO FW14_SCHPO FW14_SCHPO FW14_SCHPO TUG_ARATH GBB_WALZE TUPT_YEAST PRP4_ARATH
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ALIGNMENTS

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL, BC032708, AH32708.1, -.
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TISSUE=Lymph;
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26-OCT-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1X protein (Transducin-beta-like 1, X-linked)
TBLIX OR TBLI.
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                 Length
                                                                                                                                     -> K (IN REF. 2).
-> H (IN REF. 3).
-> Q (IN REF. 2).
0B556D2EE4BA796D CRC64;
                                                                                                                                                                               Score 2716; DB 1;
Pred. No. 1.5e-188;
1; Mismatches 1;
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         PROSITE; PS50896; LISH; 1.
PROSITE; PS0678; WD REPEARS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                  LISH.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
WD 8.
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 SMART; SM00320; WD40; 8.
                                           WD repeat.
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264
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Matches 512;
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                                                                                                                                                                                                                                  Grandi A.
MEDIINE-99264241; PubMed=10330347;
Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A. Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G.;
"X-linked late-onset sensorineural deafness caused by a deletion involving OAL and a novel gene containing WD-40 repeats.";
Am. J. Hum. Genet. 64:1604-1616(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 300196; D: hearing; TAS. GO; GO:0007665; P: hearing; TAS. GO; GO:0007165; P: signal transduction; TAS. GO; GO:0007601; P: vision; TAS. InterPro; IPR006594; LisH. InterPro; IPR001680; WD40. Pfam; PF00400; WD40. PRIMTS; PR00320; GPROTEINBRPT. PR00000; WD40; ProDom; PD000018; WD40; 3.
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SMART; SM00320; WD40; 7.
PROSITE; PSS00896; LisH; 1.
PROSITE; PSS00678; WD REPEATS 1; 4.
PROSITE; PSS0082; WD REPEATS 2; 6.
PROSITE; PSS0294; WD REPEATS 2; 6.
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23 216
23 212
74 313
6 354
7 447
489 W
521 WL
56688 MW; 4
                            EMBL; AF332220; AAK13472.1;
EMBL; AF332221; AAK13473.1;
EMBL; AF332222; AAK13474.1;
Genew; HGNC:18502; TBL1Y.
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522 AA;
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                                                                                                                                    EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAA--- 117
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                                                                      Gaps
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1 TBLY HUMAN STANDARD, PRT; 522 AA.

28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Transducin beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
Transducin Beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
Homo sapiens (Human)
Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammaila; Eutheria, Primates, Catarthini, Hominidae, Homo.
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Wilson R.K., Waterston R.H., Page D.C.;
"The DNA sequence of the human Y chromosome.";
Submitted (BCC-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 Lish domain.
-!- SIMILARITY: Contains 8 WD repeats.
                                                                     14;
                                               Length 526;
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                                                                   Indels
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POLY-ALA.
98922F88EC42F6E9 CRC64;
                                            89.4%; Score 2437; DB 1; I
86.0%; Pred. No. 2.1e-168;
ive 33; Mismatches 27;
 525 WD
124 PO
57048 MW;
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les 453; Conservative
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526 AA;
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Best Local Similarity 84.5%; Pred. No. 2.4e-163;
Matches 442; Conservative 35; Mismatches 34;
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InterPro; IPR006594; Lish:
InterPro; IPR006694; Lish:
InterPro; IPR001680; WD40.
PERMYS; PR00400; WD40.
PARNYS; PR00320; WD40; 3.
RMART; SW00667; Lish; 1.
SWART; SW00677; Lish; 1.
SWART; SW00679; WD40; 8.
PROSITE; PS50896; LISH; 1.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50082; WD_REPEATS_2; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKDVTSLDWNMEHCWQQVPMMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 NLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 GSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 QFPFHS-APALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 QFPFHSAAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTFQGHT-BVNAIKWDPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                         Botcherby M.R.M., Straw R., Clarke D., Greystrong J.S., Weston P., Hunter G., Kimberly C., Rhodes M.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: Contains at least 5 WD repeats.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 WD 1.
115 WD 2.
198 WD 3.
249 WD 4.
291 WD 5.
313
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                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1X protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1336/T2; TD11x.
InterPro; IPR001680; WD40.
PEdm; PP000400; WD40; S.
PEDOM; PP00020; GPROTEINBRPT.
PRODOM; PD000018; WD40; 2.
SWART; SW00320; WD40; 2.
PROSITE; PS00678; WD REPEATS 1; 3.
PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50294; WD REPEATS 2; 4.
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76
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160
201
252
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313 AA;
                                                                                                                                                                           musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                    TBLIX OR TBLI.
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RESULT 5 SIF2_YEAST

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. . .; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                John F. 15:2991-3004 (2001).

-! FUNCTION: Antagonizes telomeric silencing in yeast. May recruit sire nontelomeric sites or repression.

-!- SUBURT: Interacts with SIR4 amino-terminal domain. Interacts with a complex composed of SIN3 and RPD3. Identified in the Set3C complex with HOS2, HST1, SNT1, CPR1, HOS4/YIL112W and SET3.
-!- SUBCELIULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 Lish domain.
-!- SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X78993; CAA55606.1; -.

BREL; X78993; CAA55606.1; -.

BREL; X38972; CAA8508.1; -.

BREL; Z35972; CAA8508.1; -.

B PIR; S48266; S48268.

B GERMONline; 138646; -.

SGD; S0000307; SIF2.

SGD; CO.000118; Cinicleus i PI.

GO; GO:00017136; F:NAD-independent histone deacetylase activity; IDA.

GO; GO:0017136; F:NAD-independent histone deacetylase activity; IDA.

R GO; GO:0015634; P:NAD-independent histone deacetylase activity; IDA.

R GO; GO:0015575; P:Nistone deacetylation; IDA.

GO; GO:0015575; P:Nistone deacetylation; IDA.

GO; GO:0015575; P:Nistone deacetylation; IDA.

GO; GO:0015575; P:Nistone deacetylation of transcription from P. . .; IE

R GO; GO:0001687; LisH.

InterPro; IPRO01680; WD40;

R Pfam; PF00440; WD40;

R PARAT; SM00667; LisH; 1.

R SMART; SM00667; LisH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21567937; PubMed-11711434; MEDLINE-21567937; PubMed-11711434; MEDLINE-21567937; PubMed-11711434; Milm M., Rigaut G., Seraphin B., Aasland R., Stewarth A.F.; Wilm M., Rigaut G., Seraphin B., Aasland R., Stewarth A.F.; The S. cerevisiae SET3 complex includes two histone deacetylases; Hosz and Hst1, and is a meiotic-specific repressor of the sporulation gene program."
                                                                                                                                                                                                                                                                                                                                                                                                                               Cockell M., Renauld H., Watt P., Gasser S.M.; "Sif2p interacts with Sir4p amino-terminal domain and antagonizes telomeric silencing in yeast."; Curr. Biol. 8:787-790(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION IN A COMPLEX WITH HOS2; HST1; SNT1; CPR1; YIL112W
                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
                                   (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50896; LISH; 1.
PROSITE; PS00678; WD_REPEATS_1; FALSE_NEG.
                                                                                                  SIR4-interacting protein SIF2.
SIF2 OR EMB1 OR YBR103W OR YBR0832.
                                                                                                                                                                                                                                                                                           MEDLINE=95208357; PubMed=7900426;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98315485; PubMed=9651685;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                          STRAIN=S288C
                                        01-OCT-1994
                                                            01-OCT-1994
10-OCT-2003
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EMBL; AP003593; BAB75165.1; -.
BIR; AC2293; AC2239.
INTERPRO; IPR00711; NACHT_NTPASE.
InterPro; IPR001680; WD40.
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1027
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1153
11195
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Best Local Similarity
Matches 117; Conserv
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                                                                                                                                                                                                                                                                                                      Hypothetical
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                                                                                                                                                                                                         50 ISIIQKGLQYVEAEVSINEDG---TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ 106
                                                                                                                                                                                                                     51 VNLVQRGILYTESELMYDSKGDISALNEHHLSEDFNLVQALQID-----KEKFPEI 101
                                                                                                                                                                                                                                              QAAAAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLR 166
                                                                                                                                                                                                                                                                                  167 GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTQ-----LVLRHCIREGG 219
                                                                                                                                                                                                                                                                                               -KLDNIVSSTWNPLDESILAYGEXNSVARLARIVETDQEGKKYWKLTIIAELRHPFALSA 214
                                                                                                                                                                                                                                                                                                                                  215 SSGKTTNQVTCLAWSHDGNSIVTGVENGELRLWNKTGALLNVLNFHRAPIVSVKWNKDGT 274
                                                                                                                                                                                                                                                                                                                                                           FILSAGVDKTTIIWDAHTGEAKQQFPF------HSAP---ALDVDWQSNNTFAS 324
                                                                                                                                                                                                                                                                                                                                                                                               CSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV 384
                                                                                                                                                                                                                                                                                                                                                                                                           PGPKGAIFVYQITEKTPTGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSQ 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSFYGHSQSIVSASWV------GDDKVISCSMDGSVRLWSLKONTLLALSIVDGVP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 HIISMDVENVTILWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVI 334
                                                                                                                                                                                                                                                        SSEGRFTLETNSESNKAGEDGASTVERETQEDDTNSIDSSD--DLDGFVKI--LKEIV--
                                                                                                                                                                                        -----PLGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                    HDLQQHNXEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEP
                                                                                                                                                                     1 MSISSDEVNFLVYRYLQESGFSHSA------FTFGIKSHISQSNINGALVPPAAL
                                                                                                                                                                                                                                                                                                                        220 QDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGN
                                                                                                                                                   97;
                                                                                                                                DB 1; Length 535;
                                                                                                     -> C (IN REF. 1; CAAB5058).
25DD19AB2BFB4B07 CRC64;
                                                                                                                               18.4%; Score 502.5; DB 1; Length llarity 24.9%; Pred. No. 8.2e-29; Conservative 100; Mismatches 232; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
ND REPEATS 2; 4.

MD_REPRATS_REGION; 1.

Chromatin regulator; Nuclear protein.
36
                                                                                                                                                                               VYSVAFSPDGRYLASGSFDKCVHIW-----NTQTGAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
4-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein alr3466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGGIFEVCWNAAGDKVGA--SASDGSVCVL 510
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                                      WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
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257
WI
354
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473
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396
S9145 WI
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                                                                                           440
396
335 AA;
                   WD repeat;
PS50082;
PS50294;
                                                                                                                                         Similarity
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NCBI_TaxID=103690;
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                                      163
218
259
315
399
                                                                                                                             Query Match
Best Local Simi:
Matches 142; (
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QBYRI1;
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                                                                                                    CONFLICT
          PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 PALDVDWQSNNTF-----ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 NGAHTIANNHTDMMEVDGDVEIPPNKAV-VLRGHESEVFICAWNPVSDLLASGSGDSTAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1226 LWEINSSKCLCTFQGHTSWVNSVVFNPDGSMLASGSSDKTVRLWDISSSKCLHTFQGHT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanbab A., Iriguchi M., Ishikwa A., Kawashima K., Kimura T., Kibida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8.205-213 (2001).
-! SIMILARITY: Contains 1 pentapeptide repeat domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; Repeat; WD repeat; Complete proteome.
34 376 WD 1.
23 862 PENTAPEPTIDE.
52 901 WD 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1324 1363 WD 13.
1366 1405 WD 14.
1408 1447 WD 15.
1450 1491 WD 16.
1526 AA; 170376 MW; D5DF272509B4A738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.6%; Score 479; DB 1; Length 15
29.8%; Pred. No. 1.6e-26;
tive 76; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEANTS: PF00400; WD40; 15.
PRINTS: PR00220; GPROTEINBRPT.
PRODOM: P0000018; WD40; 8.
PROSITE: PS00678; WD REPEATS 1: 11.
PROSITE: PS50082; WD REPEATS 1: 11.
PROSITE: PS500824; WD REPEATS REGION; PROSITE; PS50837; NACHT; UNKNOWN.1.
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7;

Gaps

77;

224

277

397

337

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                                                                                                                                                                                                                                                                                 1153 AFSPDGK------ILASASHDQTVRIWDVNTGKCHHICIGHTHLVSSVAFSPDGEVV 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96009801; PubMed=7557402;
MEDLINE=96009801; PubMed=7557402;
Saupe S., Turcq B., Begueret J.;
Saupe S., Turcq B., Begueret J.;
A gene responsible for vegetative incompatibility in the fungus Podospora anserina encodes a protein with a GTP-binding motif and beta homologous domain.";
Deta homologous domain.";
Gene 162:135-139(1995).
- PUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH
SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED GENE,
                                                                                                                                                            165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS
                                                                                                                                                                                                                                                                                                                                               278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
                                                                                                                                                                                                                                                       225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                            338 ODRPIKTFOGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKODNCVHDLOQHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
NCBL_TaxID=5145;
                                                                    Length 1258;
                                                                                                                                                                                         974 LEGHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGQCFQILLEH-
                                                                                                                Indels
1186 1227 WD 15.
1258 AA; 139513 MW; 45DF03B91170C451
                                                                    17.0%; Score 463.5; DB 1;
Similarity 31.8%; Pred. No. 1.7e-25;
03; Conservative 44; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-ULL-1998 (Rel. 36, Created)
15-ULL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vegetatible incompatibility protein HET-E-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1356 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 10 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1204 ASGSODOTVRIWNVKTGECLOILR 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 ASGSFDKCVHIWNTQTGALVHSYR 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, L28125; AAA85775.1; -.
PIR, T18521, T18521.
InterPro; IPR007111; NACHT_NTPase.
InterPro; IPR001680; WD40.
Pfan; PP05729; NACHT; 1.
Pfan; PF00400; WD40; 10.
                                                                                                                     Matches 103; Conservative
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    REPEAT
SEQUENCE
                                                                         Query Match
Best Local (
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Q00808;
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                                                                                                                       1450
    482
                                                                                                    TVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDILIPE-2155-2985; PubMed=11759840;

KADACOT., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Kanacko T., Nakamura Y., Wolk C.P., Kuritz T., Kimura T.,

Katanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Pakazawa M., Yamada M.,

Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-!- SIMILARITY: Contains 1 NB-ARC domain.
-!- SIMILARITY: Contains 15 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00320; WD40; 14.
PROSITE; PS00678; WD REPEATS 1; 9.
PROSITE; PS50082; WD REPEATS 2; 14.
PROSITE; PS50044; WD REPEATS REGION; 1.
Hypothetical protein; Repeat; WD repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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                                                                                                                                                                      513
                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                  PRT; 1258 AA
                                                                                                                                                                      483 -TGGIFEVCWNAAGDKVGASASDGSVCVLDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical WD-repeat protein alr2800.
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InterPro; IPR001282; NB-ARC.
InterPro; IPR001680; WD40.
Pfam; PF00400; ND40; 1.
PRIM: PR00400; WD40; 14.
PRIM: PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120)
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975
1017
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1101
1143
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NCBI_TaxID=103690;
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28-FEB-2003
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Q8YTC2;
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YESO ANASP
DY ACCOMPANASP
DT 28-FEBB
DT 28-FEB
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482 GTGGIFEVCWNAAGDKVGASASD 504
     MEDLINE=21595285; PubMed=11759840;
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Best Local Similarity
Matches 109; Conserv
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REPEAT 107
REPEAT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1070 SDDHTIKIWDAVSGTCTQTLEGHGDSVWSVAFSPDGQ------RVASGSIDGTIKIW 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         950 KIWDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHG 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LEGHGGSVWSVAFSPDRERVASGSDD 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STARIWNLSENSTSGS-TQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 RIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 APALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAASQQGSAKNGE----NT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     73; Mismatches 178; Indels
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Anabaena sp. (strain PCC 7120).
Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                965FB319844E0651 CRC64;
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3.3e-25;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein all2124.
                                                                                                                                                                         (POTENTIAL)
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 10.
SMART; SM00320; WD40; 10.
PROSITE; PS50837; NACHT; 1.
PROSITE; PS50678; WD_REPEATS_1; 10.
PROSITE; PS50087; WD_REPEATS_2; 10.
PROSITE; PS50084; WD_REPEATS_2; 10.
GTP-binding; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 460;
Pred. No. 3
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WD 2.
WD 5.
WD 5.
WD 6.
WD 9.
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27.9%;
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911
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SEQUENCE FROM N.A.
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Q8YV57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 QFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDFTG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AKNGENTANGEENCAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDL
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabana sp. strain PCC 7120.";
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llarity 28.5%; Pred. No. 4.9e-24;
Conservative 69; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIE, AF2071; AF2071.
InterPro; IFR00168; WD40.
Pfam, PP00400; WD40; 14.
PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 14.
PROSITE; PS00678; WD REPEATS 1; 3.
PROSITE; PS50082; WD REPEATS 2; 14.
PROSITE; PS50294; WD REPEATS 2; 14.;
PROSITE; PS50294; WD REPEATS REGION; 1.
Hypothetical protein; Repeat; WD repeat; C
                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 13 WD repeats.
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AT TISSUE-Lung, and Placenta;

AT TISSUE-Lung, and Placenta;

A Strausberg R.L.; Feingold E.A.; Grouse L.H., Derge J.G.,

A Strausberg R.L.; Feingold E.A.; Grouse L.H., Schemen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

A Alschul S.F., Jordan H., Moore T., Max S.I., Wang J., Habte F.,

A Diatchenko L., Marusina K., Farmer A.A.; Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninot P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninot P.D., Mullahy S.J.,

Brownstein M.J., Wokernan K.J., Abramson R.D., Mullahy S.J.,

Broak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Bakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schent J.B., Jones S.J.W., Marra M.A.;

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schent J.B., Jones S.J.W., Marra M.A.;

Human and mouse CDNA sequences.";

In Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                  278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
                                                                                                                                                                                                                                                                                                   338 ODRPIKTFOGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI 397
                                                                                                                                                                                                                                                                                                                                                                                                  398 KWSPIGPGINNPNANLMLASASFDSIVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYL 457
158 PPNKAVVLRGHESEVFICAMNPVSDLLASGSGDSTARIMNLSENSTSGSTQLVLRHCIRE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
ISOGAIT., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.,
"NEDO human CDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUS7_HUMAN STANDARD; PRT; 485 AA. Q9NVZ; 060868; Q9BU54; 10-0CT-2003 (Rel. 42, created) 10-0CT-2003 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) WD-repeat protein HUSSY-07.
                                                                                                                                                                                                                                                    1518 SRYILTASVDNTARIWDF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Syneohocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                         SEÓUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D63999; BAA10064.1; -...
PIR; $76086; $76086.
InterPro; IPR0018941; TPR-like.
InterPro; IPR001899, WD40; 16.
PRINTS; PR001320; GPROTBINBRPT.
PRINTS; PR001320; GPROTBINBRPT.
PRODOM; PD00019; WD40; 16.
PROSITE; PS00678; WD REPEATS.1; 8.
PROSITE; PS50082; WD REPEATS.2; 15.
PROSITE; PS50082; WD REPEATS.2; 15.
PROSITE; PS0094; WD REPEATS.3; WD REPEA
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NCBI_TaxID=1148;
                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2011 (Rel. 40, Last annotation update)
Hypothetical WD-repeat protein $110163.
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       1612 HQAGVMSAIFSPDGKTLISGSLD 1634
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Best Local Similarity 28.5'
Matches 107; Conservative
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REPEAT 10
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ID _Y163_SYNY3
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PRINTS, PRO0319, GRECTEINBRPT.
PRODOM; DR000118, MD40, 7.
SMART; SM00320, WD40, 8.
PROSTIE; PS00678, WD REPEATS_1; 4.
PROSTIE; PS50082, WD REPEATS_2; 7.
PROSTIE; PS50294, WD_REPEATS_2; 7.
                                                                                                              446 YSVAFSPDGRYLASGSFDKCVHIW 469
                                                                                                                                 460 YAVDWSPDGQRVASGGKDKCLRIW 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein; Repeat; WD repeat.
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InterPro; IPR001632; Gprotein_B.
InterPro; IPR001680; WD40.
Ffam, PP00400; WD40.
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                           MOUSE
                 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 TDMCIHVCKLGQD-RPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEGHSEAVISVAFSPTGKYLASGSGDTTVRFWDLSTETPHFTCKGHRHWVLSISWSPDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLASGCKNGQILIWDPSTGKQVGRTLAGHSKWITGLSWEPLHANPECRYVASSSKDGSVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 DVPS----NSEGTLLATGSYDGFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QSNNTFASCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                                                                           Sanchez J.-C.,
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                                             Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
Cannata N., Zimbello R., Lanfranchi G., Valle G.;
"Characterization of 16 novel human genes showing high similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 366.5; DB 1; Length 485; Pred. No. 4.7e-19; 47; Mismatches 145; Indels 89
                                                                                                                                                                          ж.,
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                                                                                                                                                          MEDLINE=22317277; PubMed=12429849; Scherl A., Coutte Y., Deon C., Calle A., Kindbeiter K. Scherl A., Coutte Y., Deon C., Calle A., Kindbeiter K. Greco A. Hochstrasser D.F., Diaz J.-J.; "Functional proteomic analysis of human nucleolus."; Mol. Biol. Cell 13:4100-4109(2002).
-i- SUBCELINILAR LOCATION: Nuclear; nucleolar.
-i- SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSO0678; WD_REPEATS 1; 4.
PROSITE; PSSO082; WD_REPEATS 2; 7.
PROSITE; PSSO294; WD_REPEATS REGION;
Nuclear protein; Repeat; WD repeat.
                  IISSUE=Brain;
WEDLINE=21064499; PubMed=11124703;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK001320; BAA91621.1; -..
EMBL; BC002884; AAH02884.2; -..
EMBL; BC012075; AAH12075.1; -..
EMBL; AJ005257; CAA06444.1; -..
SWISS-2DBAGE; Q9VXZ; HUMAN.
InterPro; IPR001632; Gprotein_B.
InterPro; IPR001680; WD40.
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PRINTS; PROGREGE GPROTEINBRT.
PRODOM; PDOGROUB; WD40; 7.
SMART; SM00320; WD40; 8.
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282
WD
366
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409
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WD
53266 MW
SEQUENCE OF 400-485 FROM N.A.
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26.8%;
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Best Local Similarity 26.8%
Matches 103; Conservative
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                                                                                                           Yeast 18:69-80(2001).
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                                                                                                                                           SUBCELLULAR LOCATION
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485 AA;
                                                                                             yeast sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RX SETAUSPEZ 3388257; PubMed=12477932;
RX STRUSPEZ 8788257; PubMed=12477932;
RX STRUSPEZ 8788257; PubMed=12477932;
RX STRUSPEZ 878.
RA Alteschul S.F., Zeeberg B., Butcow K.H., Scheffer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Butcow K.H., Scheffer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Capleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RY, Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RR Hann and mouse CDN sequences.";
RY Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
C. -- SIWILARITY: Contains 8 WD repeats.
C. -- SIWILARITY: Contains 8 WD repeats.
DLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV 445
                                                          10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
WD-repeat protein HUSSY-07.
WLs musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinaeleostomi;
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MEDLINE=92244356; PubMed=1574125;

MEDLINE=92244356; PubMed=1574125;

Oliver S.G., van der Aart Q.J.M., Agostoni-Carbone M.L., Aigle M.,

Alberghina L., Alexandraki D., Antoine G., Anwar R., Ballesta J.P.G.,

A Benit P., Berben G., Bergantino E., Bireau N., Bolle P.-A.,

Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,

Carignani G., Chanet R., Contreras N., Crouzet M., Daignan-Fornier B.,

Carignani G., Chanet R., Endmann D., Esteban M., Fabre F.,

Dujon B., Duesterhoeft A., Erdmann D., Esteban M., Fabre F.,

Francingues-Gaillard M.-C., Franco L., Frontali L., Fukuhara H.,

Francingues-Gaillard M.-C., Franco L., Frontali L., Fukuhara H.,

Anler LJ., Gent M.E., Gigot D., Gilliquet V., Glansdorff N.,

Actat D., Hegemann J.H., Herbert C.J., Hilger F., Hohmann S.,

Hatat D., Hegemann J.H., Herbert C.J., Hilger F., Hohmann S.,

Ander C., Jacquet M., James C.M., Jannes A., Jisone K., Jackman P.,

Kleinhans U., Kreisl P., Lafranchi G., Lewis C., van der Linden C.G.,
                                                                                                                                             220
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                                                                                                                                                                                                                                                                                                                                                                                                                    409 SLRCHVAAVYQIAWSAD-----SRLLVSGSSDSTLKVWDVKAQKLATDLPGHADEV 459
                                                                                                                                                                                                                                                             230 VWDTTAGRCERILIGHTQSVTCLRWGGDG-LLYSASQDRTIKVWRAHDGVLCRTLQGHGH
                                                                                                                                                                                                                                                                                                                                                             | : : | : | : | : | | | : : | : | DETLETMSPAEDKKPLARMTGHQALINQVLFSPDSRIVASASFDKSIKLWDGRTGKYLA
                                                                                                                                               165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                                                              221 DVPS-----NSEGTLLATGSYDGFAR
                                                                                                                                                                                                                     170 KLASGCKNGQILLWDPSTGLQVGRTLTGHSKWITGLSWBPLHMNPECRYVASSSKDGSVR
                                                                                                                                                                                                                                               IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH--
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                                                                                                                                                                                                                                                                                                                                                                                              386 DLOQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV
                                                                                                                       89; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Fungi, Ascomyoota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces
                                                                                              Length 485;
                                                                                                                       Indels
                                                                        2D7F59D603AEC07B CRC64;
                                                                                                DB 1;
                                                                                                                       48; Mismatches 145;
                                                                                                Score 365.5; DB 1
Pred. No. 5.5e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 YAVDWSPDGQRVASGGKDKCLRIW 483
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WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
                                                                                                                                                                                                                                                                                                --SAPALDVDW------
                                                                        53148 MW;
                                                                                                13.4%; 26.6%;
                                                                                                                       Matches 102; Conservative
 241
282
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451
                                                                        485 AA;
                                                                                                             Similarity
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Lucchini G., Lutzenkirchen K., Maat C., Mannhaupt G., Manzano M.E.,
Martegani E., Mathieu A., Maurer C.T.C., McConnell D., McKee R.A.,
Messenguy F., Mewes H.-W., Molemans F., Montaque M.A., Navas L.,
Mewlon C.S., Olson M.V., Pallier C., Panzeri L., Pearson B.M.,
Perea J., Philippsen P., Pierard A., Planta R.J., Plavani P.,
M. Poetsch B., Pohl F.M., Purnelle B., Ramezani Rad M., Rasmussen S.W.,
Raynal A., Remacha M., Richterich P., Roberts A.B., Rodriguez F.,
Sanz E., Schaaff-Gerstenschlaeger I., Scherts B.,
Shu Y., Skala J., Slonimski P.P., Sor F., Soustelle C.,
Shejeqelberg R., Stateva L.I., Steenman B., Schweitzer B.,
A. Thirocs G., Triano L.N., Urrestenazu L.A., Valle G., Vetter I.,
A. von Wettstein D., Wicksteed B.L., Wilson C., Wurst H., Xu G.,
Zimmermann F.K., Sgouros J.G.;
II. Nature 357:38-46(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jimenez A.; .
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valles G., Volckaerts G.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 8 WD repeats.
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PRINTS; PR00319; GPROTEINB.
PRINTS; PR00320; GPROTEINBRPT.
PRODM; P0000018; WD40; 6.
PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS500294; WD_REPEATS_2; 7.
Hypothetical protein; Repeat; WD_repeat.
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PIR; S19497; S19487.
Germonline; 138973; -.
SGD; S0000668; YCR072C.
InterPro; IPR001632; Gprotein_B.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
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Matches 124; Conservative
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484
515 AA;
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                                                                                                                                                                                                             300
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----IAGHGSTILCSAFAPHTSSRMVTGAGDNTARIWDCDTQTPMH 180
                                                                   -----SWSPDGEVIATGSMDNTIRLWDPKSGQCLG 222
                                                                                                     312
                                                                                                                                                                                                  STSGSTQLVLRHCIREGGDDVPSNKDVTSLDWNSEGTLLATGSYDGFARIW-TKDGN-LA
                                                                                                     STLGQHKGPIFALKWN----KKGN--FILSAGVDKTTIIWDAHTGEAKQQFPFHSAPAL
                                                                                                                                                                                                                                                                                                                     ----NNPNANLMLASASFDSTVRLWDVDRGI-CIHTLTKHQEPVYSVAFSPDGRYLASG
                                                                                                                                                                             313 DVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMT
                                                                                                                                                                                                                                                                                 VRVWDINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFDHTGKKPSTPEEAQKKALENY
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Nuclochide sequences of Dictyostelium discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters casparagine, glutamine, or threonine.";
Mol. Gen. Genet. 218:453-459(1989)
-!- DEVELOPMENTAL STAGE: The concentration of AAC-rich mRNAs is low in dormant spores and growing cells, but increases during spore-germination and multicellular development.
-!- MISCELLANGUOUS: Several proteins derive from AAC-rich mRNA, which due to a frameshift also have ACA and CAA codons and thus are ASC. Thr. or Gln-rich.
                                                                                                                                                                                                                                                                                                                                                                                                              SFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDLR 513
                                                                                                                                         DALRGHSKWITSLSWEPIHLVKPGSKPRLASSSKDGTIKIWDTVS----
                                                                                                                                                                                                                                                 373 LKIWSM-KQDNCVHDLQQHNKEI-----YTIK---WSPTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI TaxID=44689,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN'1990 (Rel. 13, Created)
01-JAN'1990 (Rel. 13, Last sequence update)
01-YAR-2004 (Rel. 43, Last annotation update)
AAC-rich mRNA clone AAC3 protein (Fragment).
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SMART; SN00320, WD40, 5.
PROSITE; PS00679, WD REPEATS 1; 3.
PROSITE; PS50062, WD REPEATS 2; 3.
PROSITE; PS50294; WD_REPEATS 2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=90066348; Pubmed=2511421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X16524; CAA34531.1; -.
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 5.
                                                                  TLKGHYNWVL--CV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 PCRSVSFSFDGGFIAASSFESTIEIFHIESSQPIHTIE-CSGVSSLMWHPTLPLLAYAPE
                                                                                                                                                                                                        LSNNLNSNSKEST----NIPKTNTQYTNFDSKNLDLASRYFSECSTKDFIGNKKKSTSVA
                                                                                                                                                                                                                                        -TKDGNLAST - - LGQHKGPIF
                                                                                                                                                                                                                                                                                                                                     329 MCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH---
                                                                                                                                                                                                                                                                                                                                                                                     --DLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQE
                                                                                                                                                                                          180 VSDLLASGSGDSTARIWNLSENST-----SGSTQLVLRHCIREGGQD-VPSNKDVTSLD
                                                                                                                                                                                                                                                                                       271 ALKWNKKGNFIL-SAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTF-ASCSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                   PVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGIFEVCWN-----AAGDK
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                                                                                                                                                                   Gaps
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98225157; PubMed=9556563;
Johnstone R.W., Wang J., Tommerup N., Vissing H., Roberts T.,
"Ciao 1 is a novel WaPd protein that interacts with the tumor
Suppressor protein WII.";
J. Biol. Chem. 273:10880-10887(1998).
                                                                                                                                           DB 1; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Adams M.D., Loftus B.J., Zhou L., Crosby M., Fuhrmann J., Brandon R., Kim U.J., Kerlavage A.R., Venter J.C.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  Indels
                                                                                                                    7B5AE61228D0A1A9 CRC64;
                                                                                                                                          12.8%; Score 348.5; DB 1; 26.1%; Pred. No. 8.1e-18; ive 72; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
WD-repeat containing protein Ciao 1.
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WD 2.
WD 4.
WD 5.
WD 6.
WD 7.
GLN-RICH.
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                                                                                                                     49151 MW;
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421 INENNKDPSIRV 432
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                                                                                                                                                                   97; Conservative
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                                                                                                                   437 AA;
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Best Local Similarity
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CIA1_HUMAN
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or send an email to license@isb-sib.ch).
MEDLINE=22388257; PubMed=12477932;
A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A ltschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Bhat N.K.,
A platchul S.F., Zeeberg B., Buetow K.H., Schemer G.M., Hasieh F.,
A Diatchennko L., Marusina R., Farmer A.A., Rubin G.M., Hasieh F.,
Stapleton M.J., Osdra M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mullahy S.J.,
Brosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
Human and mouse cDNA sequences";
Il Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0008284; P:positive regulation of cell proliferation; TAS. GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; TAS. InterPro; IPR001689; WD40. Pfam. PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.

CHARACTERIZATION.

SPECIAL SP3367400; PubMed=10438340;

Johnstone R.W., Tommerup N., Hansen C., Vissing H., Shi Y.;

Structural organization, tissue expression, and chromosomal

"Structural organization, tissue expression, and chromosomal

"Goalization of Ciao 1, a functional modulator of the Wilms' tumor

suppressor, WTI.";

Immunogenetics 49:900-905(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Seems to specifically modulate the transactivation activity of WT1.
SUBUNIT: Interacts with WT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- SUBCELLULAR LOCATION: Nuclear.
-- MISCELLANEOUS: 'Ciao' means 'bridge' in Chinese.
-- SIMILARITY: Contains 7 WD repeats.
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PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
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EMBL, AAC04020, AAC23493.1; -.
EMBL, BCC001395; AAH01395.1; -.
EMBL, BC032812; AAH32812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00320; GPROTEINBRPT.
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SM00320; WD40; 7.
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                                                             276 KKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCK 335
                                                                                                                                                       202
222 VPSNKDVTS--LDWNSEGTLLATGSYDGFARIWTKDGN---LASTLGQ-HKGPIFALKWN 275
                                                                                                                                336 LGQDRPIKIFQGHINEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDN---CVHDLQQHNK 392
                                                                                                                                                                                                                                                                  SPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGS---V 507
                                                                                                                                                                                                                                                                                                203 DPSGORLASCSDDRTVRIWRQYLPG-------NEOG--VACSGSDPSWKCI 244
                                 11 VPAHPDSRCWFLAWNPAGTLLASCGGDRRIRINGTEGDSWICKSVLSEGHQRTVRKVAWS 70
                                                                                                                                                                                               ELYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW--DVDRGICIHTLTKHQEPVYSVAF
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                                                                                                  71 PCGNYLASASFDATTCI-------
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Job time : 18.6667 secs
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GenCore version 5.1.6
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August 9, 2004, 16:40:42; Search time 8.66667 Seconds (without alignments) 3088.161 Million cell updates/sec US-09-987-701-12 2731 1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514 OM protein - protein search, using sw model Title: Perfect score: Run on:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOMMERTES		
Result		Query					
No.	Score	Match	Length	DB	ΙD	Description	on
г		00	514	-	TBLE HUMAN	09bzk7 ho	homo sapien
Ŕ			526	Н	TBLX HUMAN		homo sapien
n		86.1	522	H	TBLY HUMAN		homo sapien
4	1304	47.7	313	Н	TBLX MOUSE	O90xe7 mu	
Ŋ			535	Н	SIF2 YEAST		saccharomyc
9	u)	7.	1526	Н	YY46 ANASP		anabaena sp
7	w		1356	٦			æ
00	•	•	1258	Н	YSOO ANASP		anabaena sp
σ	45	è.	1683	Н	YL24 ANASP		anabaena sp
10	90.	4.	1693	Н	Y163 SYNY3		->
11	75.	ω,	515	Н	YCW2 YEAST		saccharomyc
12		m	485	٦	HUS7 HUMAN		homo sapien
13	62.		485	тH	HUS7 MOUSE		mus musculu
14			437	Н	AAC3_DICDI		dictvosteli
15	34		339	Н	CIA1 HUMAN		homo sapien
1,6			742	Н	PKWA_THECU		thermomonos
17	36.		409	Н	LIS1 HUMAN		homo sapien
18	35.		409	Н	LIS1_BOVIN		μ
6 ∃ 9	35.		800	Н	T2D4_HUMAN		homo sapien
50	34.		409	П	LIS1_MOUSE		
21	31.		334	Н	WDR5 HUMAN		homo sapien
22	28.		361	Н	\sim		drosophila
23	28	12.0	909	Н	PF20_CHLRE	P93107 ch	chlamydomon
24	32	-	798	Н			saccharomyc
25			579	Н	SE10 CAEEL		caenorhabdi
12		Η.	640	Н		Ø	accharomyc
27		ή,	376	М	YKY4 CAEEL	U	caenorhabdi
28		ä	1191	H			synechocyst
29	30		643	Н	T2D4_SCHPO	Ø	chizosacch
30		ä	704	-	T2D4_DROME	യ	drosophila
31	30		678		اسا	629	emericella
32		11.1	501	-		256	
33		11.1	605	7	POF1_SCHPO	053	schizosacch

009990 caenorhabdi	O14775 homo sapien P54314 mus musculu	Q93847 caenorhabdi	P49178 zea mays (m	Q09715 schizosacch	Ogund8 schizosacch	P04901 homo sapien	O9fuv2 arabidopsis	P54311 rattus norv	040687 orvza sativ	022212 arabidopsis
LI23_CABEL	GBB5 MOUSE	YZLL CAEEL	GBB_MAIZE	TU11 SCHPO	TU12 SCHPO	GBB1 HUMAN	LUG ARATH	GBBI RAT	GBB ORYSA	PRP4_ARATH
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9. c	9 0	37	38	ტ ტ	40	41	42	43	44	45

ALIGNMENTS

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By ErgB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1X protein (Transducin-beta-like 1, X-linked)
                                                                                                                                                                                                                                                                DB 1; Length 514;
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WD 1.
WD 2.
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WD 4.
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WD 6.
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WD 7.
Y 2 - X (IN REF. 2).
X - > H (IN REF. 2).
X - > Q (IN REF. 2).
X - > Q (IN REF. 2).
W, OBS5GDZEE4BA796D CRC64;
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Pred. No. 5.7e-188;
1; Mismatches 5;
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      PROSITE; PS50896; LISH; 1.
PROSITE; PS00678; MD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

TBLIX OR TBLI.

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                                                                                                                                                                                                                                                                                                                                                                                               Trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Atlausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Atlausher R.D., Collins F.S., Wagner L., Schemen C.K., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheefer T.B., Scheefer M.B., Garcia M., Hong L., Scheefer T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullahy S.J., A., Mare S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A., Marek S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Schergen B.J., Lu X., Gibbs R.A., Willialon D.K., Muzny D.M., Schergen B.J., Lu X., Gibbs R.A., Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J.W., Marra M.A., Human and mouse cons. Sci. U.S.A., 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

I. SIMILARITY: Contains 8 WD repeats.
                                                                                                           MEDLINE-99264241; PubMed-10330347;
Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A. Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G., "X-linked late-onset sensorineural deafness caused by a deletion involving OAl and a novel gene containing WD-40 repeats.";
Am. J. Hum. Genet. 64:1604-1616 (1999).
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS0082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
Repeat; WD repeat.
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EMBL, BC032708; AAH32708.1; -.
Genew; HGNC:11585; TBL1X.
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PRINTS; PR00320; GPROTEINBRPT.
PLODOM; PD000018; WD40; 3.
SMRAT; SM00667; LiSH; 1.
SMART; SM00320; WD40; 7.
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276
318
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                                        NCBI_TaxID=9606;
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us-09-987-701-12.rsp

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                                                                                                                            61 EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAAT-- 118
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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Transducin beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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                                            Length
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"The DNA sequence of the human Y chromosome.";
Submitted (DEC-2000) to the EMBJ/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 LisH domain.
-! SIMILARITY: Contains 8 WD repeats.
           POLY-ALA.
98922F88EC42F6E9 CRC64;
                                        ; Score 2439; DB 1; 1; Pred. No. 2.5e-169; 33; Mismatches 27;
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Mammalia; Butheria; Primates;
NCBI_TaxID=9606;
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86.0%;
                                      Query Match
Best Local Similarity 86.0
Matches 453; Conservative
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115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AATWTPAAISQONPPKNREATVNGEENGAHEI-NNHSKPWEIDGDVEIPPNXATVLRGHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 SEVFICAMNPVSDLLVSGSGDSTARIMNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 TIIWDAHTGEAKQQFPFHSAPALDVDWQNNMTFASCSTDMCHVCRLGCDHPVKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AATNOOGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 TIIWDAHTGBAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 NSSIMLASASFDSTVRLWDVEQGVCTHTLMKHQEPVYSVAFSPDGKYLASGSFDKYVHIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 SLDWNSDGTLLAMGSYDGFARIWTENGNLASTLGOHKGPIFALKWNKKGNYVLSAGVDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 NEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 NANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 NEVNAIKWDPSGMLLASCSDDWTLKIWSMKQDACVHDLQAHSKEIYTIKWSPTGPATSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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WD 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 NIQSGSLVHSYQGTGGIFEVCWNARGDKVGASASDGSVCVLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.1%; Score 2351; DB 1;
83.9%; Pred. No. 5.9e-163;
ive 35; Mismatches 37;
                         email to license@isb-sib.ch)
                                                                                                                                                                                                                                                              i
                                                                                                                                                                                                                                                                                                                                                                                                                                           56688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           522 AA;
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                                                                                                                                                                                                                                                                              WD repeat.
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PRT;

STANDARD;

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STANDARD;
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                            01-OCT-1994 (
01-OCT-1994 (
10-OCT-2003 (
SIF2 YEAST
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 NILASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEG-----TLLAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 QEYG-----QKSNLASTLGQHKGPIFALKWNKKGNYILSAGVDKTTIIWDAHTGEAKQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFPFHS-APALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKDVTSLDWNWEHCWQQVPMWVL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 GSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 STVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botcherby M.R.M., Straw R., Clarke D., Greystrong J.S., Weston Hunter G., Kimberly C., Rhodes M.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains at least 5 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.7%; Score 1304; DB 1; Length 313; 83.2%; Pred. No. 2.3e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1X protein (Fragment).
TBLIX OR TBLI.
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16; Mismatches
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Pfam; PP00400; WD40; S.
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD0000118; WD40; S.
SMART; SM00320; WD40; S.
PROSITE; PS00608; WD REPEATS_1; 3.
PROSITE; PS50082; WD REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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MD 2.
MD 3.
MD 4.
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Best Local Similarity 83.25
Matches 242; Conservative
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313 AA;
                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; WD repeat.
                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=129/SvJ;
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SEQUENCE
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RESULT 5 SIF2_YEAST

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10 STRP YEARS STANDARD, PRIF, 515 AA.

P19252.

DIO COCT-1994 [Rel. 130, Created)

DIO COCT-1994 [Rel. 130, Late Sequence update)

DIA STRING PROM NA.

DIA STRING PRO
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136
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                                                                                                                                                                                              VEAEVSINEDG----TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAA 116
                                                                                                                                                                                                          344 YQITEKTPIGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSPYGHSQS 403
                                                                                                                                                                                                                                                                                                                                                                                                              453
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATNOCESAKNGENTANGEENGAHTIANNHTDMM-EVDGDVEIPSNKAVVIRGHESEVFIC 175
                                                                                                                                                                                                                                                 110 ETNSE-SNKAGEDGASTVERETQEDDTNSIDSSDDLDGFVKI--LKEIV---KLDNIVSS 163
                                                                                                                                                                                                                                                                                   164 TWNPLDESILAYGEKNSVARLARIVETDQEGKKYWKLTIIAELRHPFALSASSGKTTNOV 223
                                                                                                                                                                                                                                                                                                     TSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGOHKGPIFALKWNKKGNFILSAGVDK 288
                                                                                                                                                                                                                                                                                                                TCLAWSHDGNSIVTGVENGELRLWNKTGALLNVLNFHRAPIVSVKWNKDGTHIISMDVEN 283
                                                                                                                                                                                                                                                                                                                                       TIIMDAHTGEAKQQFPF------HSAP---ALDVDWQSNNTFASCSTDMCIHV 333
                                                                                                                                                                                                                                                                                                                                                                          CKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VHSYRGTGGIFEVC 490
                                                                                                                                                                     1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNIN-GALVPPAALISIIQKGLQY
                                                                                                                                                                                                                                                                  176 AWNPVSD-LLVSGSGDSTARIWNLSENSTSGPTQ-----LVLRHCIREGGQDVPSNXDV
                                                                                                                                                                                                                                                                                                                                                        284 VTILWNVISGTVWQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFV
                                                                                                                                                                                                                                                                                                                                                                                                            IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD
                                                                                                                                                                                                                                                                                                                                                                                                                            IVSASWV------GDDKVISCSMDGSVRLWSLKONTLLALSIVDGVPIFAGRISOD
                                                                                                                                             Gaps
                                                                                                                                           79;
                                                                                                                          DB 1; Length 535;
                                                                                               -> C (IN REF. 1; CAA85058)
25DD19AB2BFB4B07 CRC64;
WD_REPEATS_2; 4.
WD_REPEATS_REGION; 1.
Chromatin regulator; Nuclear protein.
36
                                                                                                                                            Mismatches 239; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                               GRYLASGSFDKCVHIW-----NTQTGAL------
                                                                                                                         18.4%; Score 501.5; DB 1 25.4%; Pred. No. 6.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
WD-repeat protein alr3466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1526 AA
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                                   WD 1.
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                                                                                                                                          Matches 143; Conservative 101;
                                                                                                         59145 MW;
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479
396
                                  2208
2057
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3058
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535 AA;
PS50082; W
                  WD repeat;
                                                                                                                        Query Match
Best Local Similarity
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                                    163
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Anabaena sp.
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Q8YRI1;
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28-FEB-2003
                                                                                             CONFLICT
PROSITE;
PROSITE;
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                   Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 -TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1228 EINSSKCLCTFQGHTSWVNSVVFNPDGSMLASGSSDKTVRLWDISSSKCLHTFQGHT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 IWNLSENSTSGPTQLVLRHC--IREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1184 LWDISSSK------CLYILOG-----HTSWVNSVVFNPDGSTLASGSSDQTVRLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 LDVDWQSNNTF-----ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLL
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                     Kaneko I., Nakamura Y., Wolk C.P., Kuritz I., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kibida Y., Kohara M., Matsumoto M., Matsumoto M., Muraki A., Nuraki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabara S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213 (2001).
I- SIMILARITY: Contains 16 WD repeats.
I- SIMILARITY: Contains 1 pentapeptide repeat domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD_repeat; Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D5DF272509B4A738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.6%; Score 481; DB 1;
llarity 30.3%; Pred. No. 8.6e-27;
Conservative 77; Mismatches 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WD 1.
PENTAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEGN, PRO0400, WD40; 15.
PRINTS; PR00120; GPROTEINBRPT.
PRODOM; PR000018; WD40; 8.
SYART; SW00320; WD40; 15.
PROSITE; PS00678; WD REBEATS 1; 11.
PROSITE; PS50082; WD REBEATS 1; 11.
PROSITE; PS50083; WD REBEATS REGION; 1.
MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; AC2239; AC2239.
InterPro; IPR007111; NACHT NTPase.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1405 WD 14
1447 WD 15
1491 WD 16
4, 170376 MW; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP003593; BAB75165.1;
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REPEAT
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Best Local Simi
Matches 118;
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130

Gaps

68;

Indels

Length 1356;

904

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                951 IWDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHGG 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1071 DDHTIKIWDAVSGTCTQTLEGHGDSVWSVAFSPDGQ------RVASGSIDGTIKIWD 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1122 AASGTCTQTLEGHGGWVHSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEGHGGWVQ 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                 STARIWNLSENSTSGPTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFAR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     905 KTIKIWDAASGTC---TQTLEGH----GGR-----VQSVAFSPDGQRVASGSDDHTIK 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 VDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGG-IF 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAAATNQQGSAKNGE-----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWD
                                                                                                                                                                                                                                          820 İSTISVVEAEWNACTÖT-----LEGHGSSVLSVAFSADGORVASGSDDKTIKIWDT
                                                                                                                                                                                                                                                                                                        131 ANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAWNPVSDLLVSGSGD
                                                                                                                                                                                                                                                                                                                                               310 PALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCS
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.,

"Complete genomic sequence of the filamentous nitrogen-fixing

cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).

-: SIMILARITY: Contains 1 NB-ARC domain.

-: SIMILARITY: Contains 15 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
1356 AA; 149765 MW; 965FB319844E0651 CRC64;
                                                          16.9%; Score 462; DB 1; L 27.3%; Pred. No. 1.7e-25; ive 74; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical WD-repeat protein air2800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 EVCWNAAGDKVGASASDGSVCVLD
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                                                                                                                                  Conservative
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Q8YTC2;
                                                                                                     Best Local Sim
Matches 121;
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         SEQUENCE
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             1452
                                                                                                        RLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-T 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sape S. Turod B., Begueret J.;

"A gene responsible for vegetative incompatibility in the fungus Podosporal anserina encodes a protein with a GTP-binding motif and G beta homologous domain.";

Gene 162:133-139 (1995).

-i- FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED GENE,
                                                                                                                                            1393 RIMSISSGKCLYTLQGHNNWVGSIVFSPDGTLLASGSDDQTVRLWNISSGECLYTLHGHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 34), Last annotation update)
Vegetatible incompatibility protein HET-E-1.
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                                                                                                                                                                                                                                                                       : | ::: | :: | 1882
1453 NSVRSVAFSSDGLILASGSDDETIKLWDVK 1482
                                                                                                                                                                                                                                    484 GGIFEVCWNAAGDKVGASASDGSVCVLDLR 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1356 AA.
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-!- SIMILARITY: Contains 1 NACHT domain.
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PROSITE; PS50837; NACHT; 1.
PROSITE; PS508678; WD REPEATS_1; 10.
PROSITE; PS50082; WD REPEATS_2; 10.
PROSITE; PS50294; WD REPEATS_EGION; 1.
GTP-binding; Repeat; WD repeat.
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PIR; T18521; T18521
InterPro; IPR007111; NACHT INTPASE.
InterPro; IPR0071680; WD40.
Pfam; PP05729; NACHT; 1.
Pfam; PP00400; WD40; 10.
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAWNPVSDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 SYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 QFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                               Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F7CB361FF54F7137 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 451; DB 1;
Pred. No. 1.5e-24;
                                                                                                                                                                                          cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-!- SIMILARITY: Contains 13 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 1.5e-e. 28.5%; Pred. No. 1.5e-e. '''e. 71; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00400; WD40; 14.
PRINTS, PR00320; GPROTEIBREPT.
SMART; SN00320, WD40; 14.
PROSITE; PS00678; WD_REPEATS_1; 3.
PROSITE; PS50042; WD_REPEATS_2; 14.
PROSITE; PS50094; WD_REPEATS_REGION; 1.
Hypothetical protein; Repeat; WD repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1290 SSDGKAIASASRDNTIKLWNRHGIELE
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     MEDLINE=21595285; PubMed=11759840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP003588; BAB73823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JR; AF2071; AF2071.
hterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 28.5
Matches 109; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 LRGHESEVFICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LRGHSNRVYSAIFSPNGEIIATCSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEGHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGQCFQILLEH------
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                 PIR, AI2155, AI2155.
InterPro; IPR00180; WD-40.
InterPro; IPR00180; WD-40.
Pfam; PF00400; WD-40, 14.
Pfam; PF00400; WD-40, 14.
PRINTS; PR00320; GRROTEINBRPT.
PRODOM; PD000018; WD-40; 14.
PROSITE; PS0500678; WD-40; 14.
PROSITE; PS0500678; WD-REPEATS 1; 9.
PROSITE; PS050082; WD-REPEATS 2; 14.
PROSITE; PS050082; WD-REPEATS RECION; 1.
HYDOThetical protein; Repeat; WD repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1258;
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; Pred. No. 2.4e-25;
44; Mismatches 101; Indels
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein all2124.
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31.5%;
  AP003590; BAB74499.1;
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es 102; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79; Gaps
                                                                                                                                                                 SEÇUENCE FROM N.A.

MEDILINES 26127529; PubMed=8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocyetis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                         EMBL; D63999; BAA10064.1; -.

"InterPro; IPRO08941; TPR-like.

InterPro; IPRO08941; TPR-like.

InterPro; IPRO08941; TPR-like.

InterPro; IPRO08941; TPR-like.

PRINTS; PRO0120; GPROTEINBRPT.

PROMO120; PRO0181; MD40; 13.

SWART; SM00320; WD40; 13.

SWART; SM00320; WD40; 13.

PROSITE; PS00678; WD REPEATS 1; 8.

PROSITE; PS50294; WD REPEATS 2; 15.

PROSITE; PS50294; WD REPEATS REGION; 1.

PROSITE; PS50294; WD REPEATS REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0977A827A0251CFF CRC64;
                                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 390.5; DB 1;
; Pred. No. 3.6e-20;
53; Mismatches 137;
                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Hypothetical WD-repeat protein sll0163.
                                                                                                                                                                                                                                     Res. 2:153-166(1995).
SIMILARITY: Contains 16 WD repeats.
1612 HQAGVMSAIFSPDGKTLISGSLD 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189935 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%;
28.5%;
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                                                        STANDARD;
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1616
1657
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1693 AA;
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                                                                                                                                                                                                                            region from map
DNA Res. 2:153-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504
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15-JUL-1998
                                                         Y163 SYNY3
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RR STRAIN-S2886;

RATAIN-S2886;

RATAIN-S28436; Pubbed=1574125;

RATAIN-S28486;

RATAIN-S28436; Pubbed=1574125;

RA Alberghina L. Altexandraki D., Antoine G., Anwar R., Bailesta J.P.G.,

RA Benit P., Berben G., Bergantino E., Biteau N., Bolle P.-A.,

RA Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,

RA Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,

RA Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,

RA Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,

RA Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,

RA Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buller J., Doirac B.,

RA Fathread C.A., Faye G., Feldmann D., Esteban M., Fabre F.,

RA Fuller L.J., Gent M.E., Gigot D., Gilliquet V., Glansdorff N.,

RA Fuller L.J., Gent M.E., Gigot D., Gilliquet V., Glansdorff N.,

RA Hatat D., Hegmann J.H., Herbert C.J., Hilger F., Hohmann S.,

RA Hatat D., Hagmann J.H., Herbert C.J., Jia Y., Jümenez A.,

RA Hetat D., Jacquet M., Janes C.M., Jauniaux J.-C., Jia Y., Jümenez A.,

RA Kleinhans U., Zradisl P., Lafranchi G., Mannhaupt G., Manzano M.E.,

RA Kleinhans U., Kreisl P., Lafranchi G., Monnaugue M.A., Navas D.,

RA Messenguy F., Mewes H.-W., Molarer C.T. C., Monconnell D., McKee R.A.,

RA Messenguy F., Mewes H.-W., Molamans F., Montague M.A., Navas D.,

RA Raynal A., Remacha M., Richterich P., Soberts A.B., Rodriguez F.,

RA Schaeff Censtenschlaeger I., Schernens B., Schweitzer B.,

RA Shireson B., Pohl F.M., Purnelle B., Ramezani R.J., Plevani P.,

RA Shareson B., Pohl F.M., Purnelle B., Ramezani A., Schaeff Censtenschlaeger I., Scherner B., Warmington J.,

RA Thireso G., Triann L.N., Urrestarazu L.A., Valle G., Vetter I.,

RA Jimermann P. K., Sgourcs J.G.;

RA Zimermann P. K., Sgourcs J.G.;

RA Zimermann P. K., Sgourcs J.G.;

RIFER T. Mature 357:38-46(1992).
                                                       1415 -- KKLIVLRGHQDAVLNVR-SSPDSQYIVTASKDGTARVWN-----NTGRELAVLRH---- 1463
                                                                                                                                                                                                                                                                      -----YEKNIFAAEFSADQPIVTASDDNTAGIWEIVGREVGICRGHEGPVYFAQFSAD 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1595 DWSPDGQ------MLVTASNDGTARLWDLS-GRELLTLEGHGNWVRSABFSPDGRWV 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LG 1537
                                                                                                                                                                                                                                                                                                                                                                                278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
158 PSNKAVVLRGHESEVFICAMNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIRE 217
                                                                                                                                                                                          218 GGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 ODRPIKTFQCHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
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Bukaryota, Pungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCW2 YEAST STANDARD; PRT; 515 AA. B25382, Q8NKJ4; CL-MY-1992 (Rel. 22, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Hypochetical WD-repeat protein YCR072C. YCR072C.
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Cannata N.
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 NVGGALRVPGA---ISEKQLEELLNQLNGTSDDPVPYTFSCTIQGKKASDPVKTIDITDN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 VMPDVVQTRQQAYRDKLAQQHAAAAAAAATNQQGSAKNGENTANGEENGAHTIANNHT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 DMMEVDGDVEIPSNKAVVLRGHESEVFICAWNP-VSDLLVSGSGDSTARIWNLSENSTSG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 PMHTLKGH-----YNWVLCVSWSPDGEVIATGSMDNTIRLWDPKSGQCLGDALR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 QHKGPIFALKWN-----KKGN--FILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDW 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 QSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDFTGNLLASCSDDMTLKIW 376
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Pred. No. 8.8e-20;
5; Mismatches 167; Indels
                                 Jimenez A.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                   Valles G., Volckaerts G.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04451B0C38FB5318 CRC64;
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Germonline; 138973; --
InterPro; IPR001662; Gprotein_B.
InterPro; IPR001680; Wb40.
PRINTS; PR00319; GPROTEINB.
PRINTS; PR00320; GPROTEINB.
PROMODON; PD000018; Wp40; 6.
SWART; SM00320; WD40; 8.
PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS00629; WD_REPEATS_1; 5.
PR
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WW WD 2.
WW WD 4.
WD 5.
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515 AA;
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                                                                                    REVISION TO 444.
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EXECUBLINE FROM N.A.

TISSUELLUNG, and Placenta;

XX MEDLINE=22388257; PubMed=12477932;

RETURNETE-LUNG, ELLY, Carcuse L.H., Derge J.G.,

RETURNETER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIGHTH S.F., Zeeberg B., Bartow K.H., Schaefer C.R., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Bartow K.H., Schaefer C.R., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Brantsian M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brank S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RIchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RILlalon D.K., Munny D.M., Scdergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Butterfield Y.S.N., Krzywinski, M.I., Salaka W.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. "Generation and initial analysis of more than 15,000 full-length
                                                                                      464
                                                                                                                                                                    424
305 DINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFDHTGKKPSTPEEAQKKALENYEKIC 364
                                                                                                                                          365 KKNGNSEEMWVTASDDYTWFLWNPLKSTKPIARMTGHOKLVNHVAFSPDGRYIVSASFDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22317277; PubMed=12429849; Scherl A., Coute Y., Deon C., Calle A., Kindbeiter K., Sanchez J.-C., Greco A., Hochstrasser D.F., Diaz J.-J.; "Functional proteomic analysis of human nucleolus.";
                                                                                      - NNPNANLMLASASFDSTVRLWDVDRGI-CIHTLTKHQEPVYSVAFSPDGRYLASGSFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Σ ω
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Jannata N., Zimbello R., Lanfranchi G., Valle G.;
"Characterization of 16 novel human genes showing high similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M. Takabashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Inayanagi T., Inayanagi T., Inayanagi T., Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryofa, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  513
                                                                                                                                                                                                                                                                                                 SIKLWDGRDGKFISTFRGHVASVYQVAWSSDCRLLVSCSKDTTLKVWDVR 474
                                                                                                                                                                                                                                                  465 CVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NVX2; O60868; Q9BU54;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
MD-repeat protein HUSSY-07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA se
Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yeast sequences.";
Yeast 18:69-80(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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485 AA

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412
454
485 AA;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       WCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                        TISSUE=Lung;
HUS7 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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DDT THE LETT THE TEST TO DESCRIPTION OF THE PRESENCE OF THE PR
                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 WVNTMALSTDYALRTGAFEPAEASVNPQDLQGSLQELKERALSRYNLVRGQGPERLVSGS
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MOl. Biol. Cell 13:4100-4109(2002).
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMAKK; DUNUSZU, TZ., TZ., PROSTIE; PS00678; WD_REPEATS_1; 4. PROSTIE; PS50082; WD_REPEATS_2; 7. PROSITE; PS50294; WD_REPEATS_REGION; 1. Nuclear protein; Repeat; WD_repeat.
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460 YAVDWSPDGQRVASGGKDKCLRIW 483
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                                                                                                                                                                                                                                                                                                                  EMBL; AK001320; BAA1661.1; ---
EMBL; BC02884; AAH02884.2; ---
EMMBL; AC012075; AAH12075.1; ---
EMBL; AU005257; CAA06444.1; ---
SWISS-2DPAGE; Q9NVX2; HUMAN.
InterPro; IPR001632; Gprotein_B.
InterPro; IPR001632; Gprotein_B.
Pfan; PP00400; WD40; B.
PRINTS; PR00119; GPROTEINB.
PRODOM; PD0000118; WA40; 7.
SWART; SMO320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WD 23. WD 4. WD 4. WD 5. WD 6.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 WI
53266 MW;
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4atches 102; Conservative
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485 AA;
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TO COTT-2003 (Rel. 42, Created)
DT 10.0CT-2003 (Rel. 42, Last sequence update)
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                                                                                                                                                                                                                                                                                       348
                                                                                                                                                                                                                                                                                                                                        385
                                                                                                                                                                                                                                                                                                                                                                 349 DDFTLFLWSPAEDKKPLARMTGHQALINQVLFSPDSRIVASASFDKSIKLWDGRTGKYLA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLRGHVAAVYQIAWSAD-----SRLLVSGSSDSTLKVWDVKAQKLATDLPGHADEV 459
                                                                                                                                                                                                                                                                                                                                                                                                                              386 DLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV 445
LEGHSEAVISVAFSPTGKYLASGSGDTTVRFWDLSTETPHFTCKGHRHWVLSISWSPDGK 169
                                                                                                                                         251 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH-- 307
                                                                            --SAPALDVDW----OSNNTFASCS
                                                                                                                                                                                                                                                                                     289 WINTMALSTDYALRTGAFEPAEATVNAQDLQGSLKELKERASSRYNLVRGQGPERLVSGS
                                                                                                                                                                                                                                                                                                                                   TDMCIHVCKLGQD-RPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH
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"Nucleotide sequences of Dictyostelium discoideum developmentally
"Nucleotide sequences of Dictyostelium discoideum developmentally
asparagine, glutamine, or threonine.";
Mol. Gen. Genet. 218:453-459 (1989)
-!- DEVELOPMENTAL STAGE: The concentration of AAC-rich mRNAs is low
in dormant spores and growing cells, but increases during
spore-germination and multicellular development.
-!- MISCELLANEGUS: Several proteins derive from AAC-rich mRNA, which,
due to a frameshift also have ACA and CAA codons and thus are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                -----NKDVTSLDW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN'1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-YAR-2004 (Rel. 43, Last annotation update)
AAC-rich mRNA clone AAC3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AA.
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SWART; SW00320; WD40; 5.
PROSITE; PS00678; WD REPEATS_1; 3.
PROSITE; PS50082; WD REPEATS_2; 3.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asn-, Thr- or Gln-rich.
SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            446 YSVAFSPDGRYLASGSFDKCVHIW:469
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InterPro, IPR001680, WD40.
Pfam, PF00400, WD40; 5.
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P14197;
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AAC3_DICDI
DAC P14197
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                                                                                                                                                                                                                                                                                                                                                                                                         153 GDVEIPSNKAVVLRGHESEVFICAMNPVSDLLVSGSGDSTARIWNLSENST----SGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NSNSKEST----NIPKTNTOYTNFDSKN
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                                                                                                                                                                                                                                                                                                                                                                28 OTOVOOLHNOLHOOHOOLOOOAOATOOHLOTOOYLOSOIHOOSOOSOLSNN-----
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                                                                                                                                                                                                                                                                                    Gaps
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                    96;
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                                                                                                                                                                                                                                           Length 437;
                                                                                                                                                                                                  7B5AE61228D0A1A9 CRC64;
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                                                                                                                                                                                                                                                                                  79; Mismatches 175;
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1.3e-18;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
WD_repeat containing protein Ciao 1.
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                                    WD 1.
WD 2.
WD 3.
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WD 5.
WD 6.
WD 7.
GLN-RICH.
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                         161
125 227
729 266
59 308
5 355
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456 FA
75 GL
49151 MW; 75
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Mammalia; Eutheria; Primates;
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Matches 109, Conservative
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Adams M.D., Loftus B.J
Brandon R., Kim U.J.,
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WD repeat
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                             TISSUEBLOOD, ABOUND. A.

TISSUEBLOOD, AN A.

TISSUEBLOOD, AN A.

TISSUEBLOOD, AN A.

REDINE=22388257; PubMed=12477932;

RICHINE=22388257; PubMed=12477932;

RICHINE=22388257; PubMed=12477932;

RICHINE=22388257; PubMed=12477932;

RICHINE F. L., Feligoold E. A., Grouse L. H., Schamen C. M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Rapa S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Rotrigues S., Sanchez A., Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length U.P., Co. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008284; P:positive regulation of cell proliferation; TAS. GO:0006857; P:regulation of transcription from Pol II pro. . .; TAS. InterPro; IPR001680; WD40. Peam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnstone R.W., Tommerup N., Hansen C., Vissing H., Shi Y., "Structural organization, tissue expression, and chromosomal localization of Ciao 1, a functional modulator of the Wilms' tumor suppressor, WTI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenetics 49:900-905(1999).
-!- FUNCTION: Seems to specifically modulate the transactivation activity of WT1.
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63A8D8257A204FC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Interacts with WT1.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANBOUS: 'Ciao' means 'bridge' in Chinese.
-!- SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00678; WD REPEATS_1; 1.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD REPEATS_REGION; 1.
Repeat; WD repeat; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
MEDLINE=99367400; PubMed=10438340;
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ProDom; PD000018; WD40; 2.
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EMBL;
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                                                                                                                                                                                                                                                              -----TLEGHENEVKSVAWAPSGNLLATCSRDKSVWVWEVDEEDEYECVSVLNSHTQ 151
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                                                                                                            EIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW--DVDRGICIHTLTKHQEPVYSVAF
                                                                                                                                                                                            ------WKKNODDFECVT-----
      Length 339;
  Score 349; DB 1;
Pred. No. 4.2e-18;
3; Mismatches 88
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12.8%; Sco:
30.4%; Pre-
ttive 43;
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                                             92; Conservative
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Job time : 9.66667 secs
      Query Match
Best Local Similarity
Matches 92; Conserv
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

Run on:

August 9, 2004, 16:39:47; Search time 48 Seconds (without alignments) 3025.613 Million cell updates/sec

US-09-987-701-12 2731 1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514

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1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

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length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* 1: qeneseqp1980s:* geneseqp1980s:* geneseqp1990s:* geneseqp2001s:* geneseqp2002s:* geneseqp2000s: geneseqp2004s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab95225 Human pro	7190 Human p5	Add14051 Human src	Abp41760 Human ova	424	376	351 Novel	385	1350 Novel		33774 Protei	Adal3321 Human int	81	59486 Drosophi	0	'8 Drosophi	₩	Aab68516 Human GTP	928	7306 Novel	3282	93	3119 Ara	95040	Aag48120 Arabidops
OI	AAB95225	19	ADD14051	ABP41760	ABP51424	337	ABG21351	AAC04385	Ŋ	ABR52980	ABR53774	ADA13321	AAR85881	ABB59486	ABB62260	AAY79678	AAB68284	AAB68516	AAB92844	ABB97306	AAB68282	189	AAG48119	ADB95040	AAG48120
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ALIGNMENTS

Human; primer; detection; diagnosis; antisense therapy; gene therapy. Ë Saito K, , Otsuki Hayashi K, S A, Nagai K, Human protein sequence SEQ ID NO:17352. AAB95225 standard; protein; 514 AA Isogai T, Nishikawa T, Sugiyama T, Wakamatsu 27.AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776. 02-MAY-2000; 2000JP-00183767. 09-JUN-2000; 2000JP-00241899. 99JP-00248036. 28-JUL-2000; 2000EP-00116126. (first entry) (HELI-) HELIX RES INST. 29-JUL-1999; EP1074617-A2. Homo sapiens. 26-JUN-2001 07-FEB-2001. Ota T, Is Ishii S, AAB95225; RESULT 1 AAB95225

ņ Yamamoto

WPI; 2001-318749/34.

Primer sets for synthesizing polynuclectides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 8; SEQ ID NO 17352; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

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sequence and an oligonucleotide comprising a sequence complementary to a polymucleotide which comprises a 3' end sequence, where the oligonucleotide comprises at least is nucleotides and the combination of the 5'-end sequence, selected from those defined in the specification. The primer sets can be used in antisense therapy and in particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13742 represent human cond sequences; and AAH13629 to AAB92446 to AAB95893 represent human amino acid sequences, and AAH13629 to AAH3362 represent oligonucleotides, all of which are used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                      Score 2691; DB 4;
Pred. No. 2.5e-245
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                              present invention
                                                                                                                                                                                                                                                                                                   Sequence 514 AA;
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The invention relates to identifying (MI) a candidate ps. pathway in modulating agent, by contacting an assay system comprising a purified HW polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nuclaic acid with a test agent under conditions, where but correct the presence of the test agent, the system provides a reference activity, and detecting a test agent, the system provides a reference activity, and detecting a test agent, the system provides a reference activity, and detecting a test agent, the system provides a reference. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising while a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising: (a) obtaining a biological sample contacting the sample with a probe for HM expression; (c) comparison indicates a likelihood disease). (M1) is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Conditionators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to proliferation disorders (e) cancer). Another two new methods (M2 and M3) are useful for modulating the p53 pathway of a cell, thus restoring the p53 pathway of a cell, cyle p53 function of the cell, so that the cell undergoes normal conserving the p53 function or progression through the cell undergoes normal conserving the p53 pathway such as angiogenic, apsorbetic or cell proliferation disorders. The present sequence conserving the p53 pathway such as angiogenic, represents a human p53 pathway modifying protein
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                                                                                                                                                                                                                                                                                                                                                                                                  Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
                                                                                                                                                                                                                                                                                               Funke RP;
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Pred. No. 4.7e-245;
1; Mismatches 6;
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                                                                                                                                                                                                                                                                                               Belvin M,
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                                                                                                                                                               05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                         03-JUN-2002; 2002WO-US017382.
                                                                                                                                                                                                                                                                                             Friedman L, Plowman GD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathway in Drosophila.
                                                                                                                                                                                                                                                    (EXEL-) EXELIXIS INC
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                                      WO200299122-A1.
Homo sapiens.
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                                                                                       KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIKWDPT
 SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                             ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKQNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                          GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                      ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                      KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                                                                   GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                                                 DSTVRLWDVDRGICIHTLTKHOEPVYSVAFSPDGRYLASGSFDKCVHIWNTOTGALVHSY
                                                                                                                                                                                                                                                                                                                                                                                         predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                               RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                    RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                                                                                                                                    Human src biomarker polypeptide SEQ ID NO:240.
                                                                                                                                                                                                                                                                                               ADD14051 standard; protein; 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB CO.
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                                                                                                                                                                                                                                                                                                                                               entry)
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New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein Shaw P; SEQ ID NO 240; 139pp; English FY, Lee kinase pathways. Fairchild 2003-636735/60. N-PSDB; ADD14646. Claim 10; ъ, Huang

The present invention describes a predictor set comprising a plurality of the present invention describes whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase pathway. Also described: (1) predicting whether a compound is capable of modulating the activity of cells, comprising obtaining a sample of determining whether the cells comprising obtaining as ample of cells, correlating the expression of the markers to the compound's ability to modulate the activity of the cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels

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with a disease state, and (3) identifying polynucleotides and polypeptides that predict compound sensitivity or resistance of cells cells increaring the predict compound sensitivity or resistance of cells a sesociated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polynucleotides or polypeptides, and selecting pattern of polymerication of the microarray. The polynucleotides and croarray. The polynucleotides and propertides are useful in predicting the polynucleotides and polypeptides are useful in predicting the cartivity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized cancer; based on patient response at an anclecular level. The present cancer; based on patient response at an anclecular level. The present cancer; based on patient response at an anclecular level. The present cancer is used in the exemplification of the present invention.
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correlate with compound sensitivity or resistance of cells associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.3%; Score 2439; DB 7; 186.0%; Pred. No. 2.1e-221; ive 33; Mismatches 27;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 577 AA;
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ABP41760 standard; protein; 542 (first entry) 22-AUG-2002

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Human ovarian antigen HNOKM38, SEQ ID NO:2892.

Human, ovarian antigen, ovary, ovarian, breast, cancer, tumour, ovarian cancer, breast cancer, tumour; reproductive system disorder,

--NOOGSAKN 126

SLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAT

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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
infertility, pregnancy disorder, anovulation, polycystic ovary syndrome; PCOS, ovarian cyst, dysmenorrhoea; endocrine disorder; infection; infula disorder; blood disorder; infection; cardiovascular disorder, respiratory disorder; neurological disorder; gastroinestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forenoic analysis; antibody preparation; cyclostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                               07-JUN-2001; 2001WO-US018569.
                                                                                                                                                                                    07-JUN-2000; 2000US-0209467P
                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                              Birse CE, Rosen CA;
                                                                                                                                                                                                                                                  2002-147878/19.
                                                                                                                                                                                                                                                           N-PSDB; ABQ54837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 542 AA;
                                                                                                                     WO200200677-A1.
                                                                                                Homo sapiens.
                                                                                                                                         03-JAN-2002
                                                                                                                                                                                                                                                                                                                  diseases.
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The invention relates to 2175 novel human ovarian antigens (ABP41654-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identicial and polypucleotides 95% identical to to the sequences of the invention. The invention additionally relates to recombinant vectors and henceful somprising human ovarian antigen. Or recombinant vectors and not cells comprising human ovarian antigen. Or recombinant vectors and present human ovarian antigens, and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, considers. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and vaginitis), immune disorders (e.g., congenital and acquired toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and vaginitis), immune disorders (e.g., congenital and acquired conformation antigen expression or activity. The polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used for gene therapy, chromosome amapping, in the death of individuals and in forensic analysis, and the confidence data for this patent did not form part of the printed sequence cata for this patent did not form part of the printed confidence in the printed of sequence data for this patent did not form part of the printed of sequence cata for this patent did not form part of the printed of the formulation. Note: The formulation in formulation is endomed to be accounted to the printed of the printed in the formulation of the printed of the formulation of the formulation of the printed of the formulation of the formulation of the formulation of the formulation of th at ftp.wipo.int/pub/published_pct_sequences Claim 11; SEQ ID NO 2892; 2922pp; English.

4 85.8%; Score 2342; DB 5; Length 542; 85.4%; Pred. No. 2.9e-212; iive 32; Mismatches 28; Indels 14 Matches 434; Conservative Similarity

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Query Match Local

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                                                                                                                                                                            275 GFARIWTEDGNLASTLGGHKGPIFALKWNRKGNYILSAGVDKTTINDAHTGEAKQQFPF
215 GSGDSTARIWNINENSNGGSTQLVIRHCIREGGHDVPSNKDVTSLDWNTNGTLLATGSYD
                                                                                                                                                                                                                                       335 HSAPALDVDWQNNTTFASCSTDMC1HVCRLGCDRPVKTFQGHTNEVNAIKWDPSGWLLAS
                                                                                                                                                                                                                                                                                                  156 REATVNGEENRAHSV-NNHAKPMEIDGEVEIPSSKATVLRGHESEVFICAWNPVSDLLAS
                                                                                                 GSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYD
                                                                                                                                                            247 GFARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                                                                                                     HSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                  CSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRL
                                                                                                                                                                                                                                                                                                                                                              455 WDIERGVCTHTLTKHQEPVYSVAFSPDGKYLASGSFDKCVHIWNTQSGNLVHSYRGTGGI
                                      GENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAMNPVSDLLVS
                                                                                                                                                                                                                                                                                                                                           427 WDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective, antirheumatic, antiarthritic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     515 FEVCWNARGDKVGASASDGSVCVLDLRK
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05-SEP-2000; 2000US-0229748P.
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2000US-0229751P.
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06-SEP-2000; 2000US-0230595P.
06-SEP-2000; 2000US-0230597P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MDDT SEQ ID NO 446.
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05-SEP-2000;
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305 KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                        245 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                  QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEI PSNKAVVLRGHESEVFICAWNPV
                                                                     125 GGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPV
                                                                                                                                                    SDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                                                             185 SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                                                                                                                      241 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 7920; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 7920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 GNLLASCSDDMTLKIWSMKQDNCVHDLQAHN 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNLLASCSDDMTLKIWSMKQDNCVHDLQAHN 391
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila;
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ABB60376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated human disease detection and treatment (WDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 24 sequences (ABP5121-ABP5144) given in the sequence selected from 25 sequences (ABP5121-ABP5144) given in the sequence selected from 25 sequences (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound for specifically binds (I) or modulates the activity of (I) and for preparing a polyclonal or monoclonal antibody by hybridoma technology. Nucleic acids (II) (AB07244-AB07200) encocing (II) and for screening a compound for effectiveness in altering expression of a target solumning a compound for effectiveness in altering expression of a target polynucleotide comprising. Oligonucleotides and antibodies are useful for screening a compound, in a diagnostic test for a condition or a disease associated with the expression of MDDT in a biological sample, for detecting (I), an a sample, and for purifying (I) from a sample. A composition comprising (I), an associated with aberrant expression of MDDT; where the disorders are associated with aberrant expression of MDDT; where the disorders are associated with aberrant expression of MDDT, where the disorders are associated with aberrant expression of MDDT, where the disorders are associated from a cell proliferative disorder and an acid for minimatory disorder such as AIDS, Addison's disease, alternois or condition and alterny, anaemia, atherosclerosis, gout, multiple sclerosis or theumatoid arthritis. (II) are useful for creating knockin humanised and expression of more thereof is a resorder in a sample or the disorder in a sample or the formation and disease, in some the formation or more the entire or an addition or more the entire or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.
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                                                                                                                                                                                                                                                                                                                                                                                 Liu TF,
                                                                                                                                                                                                                                                                                                                                                 Jackson S, Lincoln SE, Altus CM, Dufour GE, Chalup MS; Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Dahl CK, Momiyama MG, Bradley DL, Rohatgi SD, Harris B; Roseberry AM, Gerstin EH, Peralta CH, David MH, Panzer SR, Daffo A, Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
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Pred. No. 1.1e-182;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 578; 618pp; English.
                                                                                  06-SEP-2000; 2000US-0230865P.
06-SEP-2000; 2000US-023098BP.
06-SEP-2000; 2000US-0230999P.
07-SEP-2000; 2000US-0230951P.
07-SEP-2000; 2000US-0231163P.
                            2000US-0230599P
2000US-0230610P
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98.5%;
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385; Conserv
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                                                                              06-SEP-2000; 206-SEP-2000; 206
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Best Local Si
Matches 385
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368 KLTIMTEGKRLRPKTFCSDGGALLPPAGRRPHLLTGPDIFFKRLSALFQNEVNAIKWDPS 427
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64.6%; Pred
31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                       Tang YT;
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Best Local Similarity 64.6%
Matches 368; Conservative
                                                       2001-639362/73
                                       Drmanac RT, Liu C,
                        (HYSE-) HYSEQ INC
                                                               N-PSDB; AAS85538
                                                                                                                                                                                                                                                                                                                    Sequence 584 AA;
                                                                                                        biodiversity.
                                                                                       diagnostics,
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                                   EVEWSVGEDGEV - ARPIEGLSLIDAVMPEVKPLKPIVKTEPGKPGAVDSSAPAGGNONN
                                                                                        ------QQHAAAAAAAAATNQQGSAKNGENT
                                                                                                       119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDQSASEVDSSGNAANNAGGTYAGNNG
                                                                                                                                       AGGNOASTGGSNSTSTPAGGDLAAPGASOKKSONSNEAGSSSSGNAGNANATSTDDAASS
                                                                                                                                                                 | | : :: | TSTNGNSSTSSSVEQPTSGLTPAGGTVSTSNPDAAASGGASTATGSKAPSGAVTIRVGAQ
                                                                                                                                                                                               FICAMNPVSDLLVSGSGDSTARIMNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
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                                                                                                                                                                                                                                                                                              NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNAN
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                                                                                                                                                                                       ------MEVDGDVEIPSNKAVVLRGHESEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
          77; Indels 191;
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                                                        EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRQ--
 Pred. No. 7.2e-171;
9; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #21342
                                                                                         ----QAYRDKLA-
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          49;
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 54.8%;
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          Matches 385; Conservative
  Best Local Similarity
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primeras, ollgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to a ssess biodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- AATNOOGSA
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New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Pred. No. 1.4e-169;
4; Mismatches 39;
                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 51710; 103pp; English.
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124 181 184 240 244 300 304

121 75

VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNK 392

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1 HCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFAL 60
                                                                                                              121 VCKLGODRPIKTFQGHTNEVNAIKWDPTGNILASCSDDMTLKIWSMKQDNCVHDLQAHNK
                                                                                                                                                                                                                                                                                                                                393 ELYTIKWSPTGPGTNNPNANLMLASAS 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                  480
                                                                                                                                                                                                    547
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                                         GMLLASCSDDMTLKIWSMKQDACVHDLQAHSKEIYTIKWSPTGPATSNPNSSIMLASASF
                                                                                                                                                                            DSTVRLWDVEQGVCTHTLMKHOEPVYSVAFSPDGKYLASGSFDKYVHIWNTQSGSLVHSY
      GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                      DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSY
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larity 100.0%; Pred. No. 2.4e-99;
Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                     RGTGGIFEVCWNAAGDKVGASASDGSVCVL 510
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18-MAY-2000; 2000US-00577409
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N-PSDB; AAI84316.
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      361
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence therapy techniques to restore normal setuity of (II) actorized disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders or polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutations
                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 51709; 103pp; English.
                                                                                                                            Novel human diagnostic protein #21341.
ABG21350 standard; protein; 167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT;
                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS85537
                                                                                                                                                                                                                                                                            WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biodiversity.
                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT,
                                                                                    18-FEB-2002
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                                           ABG21350;
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213 HCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFAL 272

Similarity

Best Local Sim: Matches 207;

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16;

79;

Indels

239;

DB 6; Length 535;

59 9

109 116

228 223 288

163

403

Kuester

Kruse UD,

Bauer A, Gavin A, Grandi P, Krause R, K. Marzioch M, Schultz JD, Superti-Furga GD;

WPI; 2003-250078/25.

AA ;

Sequence 535

343

Matches

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SXS

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117 ATNOQGSAKNGENTANGEENGAHTIANNHTDMM-EVDGDVEIPSNKAVVLRGHESEVFIC 175
                                                                                                                                                                                                                                                                                                                                                                                                                             TTIIWDAHTGEAKQOFPF------HSAP---ALDVDWQSNNTFASCSTDMCIHV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 CKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKE 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 IVSASWV------GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVPIFAGRISQD 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRYLASGSFDKCVHIW-----NTQTGAL-------VHSYRGTGGIFEVC 490
                                                                                                                                                              60 VEAEVSINEDG---TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAA
                                                                                                                                                                                      61 TESELMVDSKGDISALNEHHLSEDFNLVQALQID-----KEKFPE--ISSEGRFTL
                                                                                                                                                                                                                                                                                                                                                    110 ETNSE-SNKAGEDGASTVERETQEDDTNSIDSSDDLDGFVKI--LKEIV---KLDNIVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 VTILWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFV
                                                                                                         TSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 YQITEKTPTGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSQNCFYGHSQS
                                                                                                                                                                                                                                                                                                                        176 AWNPVSD-LLVSGSGDSTARIWNLSENSTSGPTQ-----LVLRHCIREGGQDVPSNKDV
                                                                               1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNIN-GALVPPAALISIIQKGLQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multiprotein complex; eukaryote; drug target; diagnosis
18.3%; Score 498.5; DB 6
25.4%; Pred. No. 8.7e-38;
ive 101; Mismatches 239
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WNCAGNKISVAYSLQEGSVVAI 535
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                                        Conservative
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                     Similarity
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                     Best Local Sim
Matches 143;
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    Query Match
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                                                                                                                                                                309
                                                                                                                                                                                                                                             369
                                                                                                                                                                                                                                                                       PALDVDWQNNMTFASCSTDMCIHVCRLGCDHPVKTFQGHTNEVNAIKWDPSGMLLAVCSD 120
                                                                                                                                                                                                       9
                                                                                                                                                                RIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAKQQFPFHSA
                                                                                                                                                                                                       RIWTENGNLAITLCQHKGPIFALKWNKKGNYVLSAGVDKTTIIWDAHTGEAKQQFPFHSA
                                                                                                                                                                                                                                           PALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSD
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                                                                                                                                                                                                                                                                                                                             DMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLA 416
                                                                                                                                                                                                                                                                                                                                                DMTLKIWSMKQEVCIHDLQAHNKEIYIIKWSPTGPATSNPNSNIMLA 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 825; 17pp + Sequence Listing; English
                                                                                 Length 167;
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multiprotein complex; eukaryote; drug target; diagnosis
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                                                                             30.2%; Score 824; DB 4; L
86.8%; Pred. No. 2.1e-69;
iive 13; Mismatches 9;
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z JD, Superti-Furga GD;
  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR52980 standard; protein; 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein sequence #SEQ ID 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                    Local Similarity 86.89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACC61022
                                        Sequence 167 AA;
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Marzioch M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2003
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                                                                                 Query Match
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N-PSDB; ACC61816.

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New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, or disorder.

To disorder.

XX

Disclosure; SEQ ID NO 2413; 17pp + Sequence Listing; English.

XX

Disclosure; SEQ ID NO 2413; 17pp + Sequence Listing; English.

XX

C the invention and DNA sequences encoding them are given in records of the invention and DNA sequences encoding them are given in records of the invention and DNA sequences encoding them are given in records or the invention and DNA sequences encoding them are given in records or the invention and DNA sequences of the protein complexes are obtainable by using a protein as a bait and isolating the set of proteins or which is attached theretof from cells. Such protein complexes may comprise to the disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on comment is available on CD-ROW

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Sequence 515 AA;
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21;
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                                                                                                                                                                                                                         --IAGHGSTILCSAFAPHTSSRMVTGAGDNTARIWDC---DTQT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------RVCQY----TMSGHTNSVSCVKWGGQG-LLYSGSHDRTVRVW 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 KKNGNSEEMMYTASDDYIMFLWNPLKSTKPIARMIGHOKLVNHVAFSPDGRYIVSASFDN 424
                                                                                                                                                                                                                                                                            ----YNWVLCVSWSPDGEVIATGSMDNTIRLWDPKSGQCLGDALR
                                                                                                                                                                                                                                                                                                                       264 QHKGPIFALKWN-----KKGN--FÌLSAGVDKTTIIWDAHTGBAKQQFPFHSAPALDVDW
                                                                                                                            87 VMPDVVQTRQQAYRDKLAQQHAAAAAAAAAAATNQQGSAKNGENTANGEENGAHTIANNHT
                                                                                                                                                                                                                                                         206 PTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIW-TKDGN-LASTLG
                                                                                                                                                                                                                                                                                                                                                                                      317 QSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIW
                                                                38 NINGALVPPAALISIIQKGLQYVEAEVSINEDGTL-----FDGR----PIESLSLIDA
                                                                                                                                                                                            147 DMMEVDGDVEIPSNKAVVLRGHESEVFICAWNP-VSDLLVSGSGDSTARIWNLSENSTSG
                                                                                                                                                                                                                                                                                                                                                       GHSKWITSLSWEPIHLVKPGSKPRLASSSKDGTIKIWDTVS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 CVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDLR 513
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Length 515;
                                85; Mismatches 167; Indels
                                                                                                                                                            101 LYSSLIKPGYNSTEDQITLLYTPRÅVFKVKPVTRSSÅ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM-KQDNCVHDLQAHNKEI-----YTIK---WSPTG--PGT-
 DB 6;
13.7%; Score 375.5; DB 6; 23.6%; Pred. No. 3.6e-26;
                                Matches 125; Conservative
                                                                                                                                                                                                                                                                                        PMHTLKGH-----
               Similarity
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 Query Match
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RESULT 12
ADA13321
LD ADA13321 standard; protein; 414 AA.
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AC ADA13321;
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AC ADA13321;
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Human intracellular signalling molecule INTSIG-3, SEQ ID NO:3.

Human; intracellular signalling molecule; INTSIG; cell proliferative disorder; cancer; atherosclerosis; autoimmune disorder; inflammatory disorder; inflection; neurological disorder; developmental disorder; endocrine disorder; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; cerebroprotective; immunosuppressive; antiinflammatory; gene therapy.

Homo sapiens.

WO2003031568-A2

17-APR-2003.

16-AUG-2002; 2002MO-US026322. 17-AUG-2001; 2001US-0313245P. 24-AUG-2001; 2001US-0316752P. 31-AUG-2001; 2001US-0316752P. 31-AUG-2001; 2001US-0316752P. 14-SEP-2001; 2001US-0326390P. 12-CCT-2001; 2001US-0326390P. 19-OCT-2001; 2001US-0345468P.

(INCY-) INCYTE GENOMICS INC

12-APR-2002; 2002US-0372499P.

Yue H, Lu DAM, Swarnakar A, Tang YT, Griffin JA, Emerling BM, Forsythe IJ, Yao MG, Ramkumar J, Richardson TW, Becha SD, Lee EA; Warren BA, Lehr-Mason PM, Baughn MR, Li JX, Duggan BM, Gietzen KJ; Lal PG, Borowsky ML, Ison CH, Thangavelu K, Xu Y, Lee S; Blliott VS, Sprague WW, Azimzai Y, Hafalia AJA, Ding L, Nguyen DB; Honchell CD, Luo W, Chawla NK, Marquis JP, Jackson JL, Tran UK;

WPI; 2003-393436/37. N-PSDB; ADA13366.

New human intracellular signaling molecules (INTSIG)), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant INTSIG expression e.g. cancer, diabetes, epilepsy, or infections.

Claim 1; Page 225-226; 367pp; English.

The invention relates to 45 human intracellular signalling molecules (INTSIG-), INTSIG-145, and the cDNAs encoding them (ADA13319-ADA13408). The invention also encompasses expression constructs, host cells and transgenic organisms comprising an INTSIG nucleic acid sequence the recombinant preparation of a INTSIG, an antibody against a INTSIG, methods of detection of INTSIG proteins or nucleic acids; a micro-array containing INTSIG nucleic acids, a micro-array containing INTSIG nucleic acids, a micro-array containing INTSIG acids, a certerior of acids; a micro-array compositions comprising a cettvity or expression; and pharmaceutical acids; acids; an INTSIG acids are useful in diagnosing, treating or preventing a variety of disorders, including cell proliferative disorders (e.g., almos allergies, anaemia, asthma, bronchitis, gout, multiple sclerosis, osteoarthritis, rheumatoid arthritis, or systemic lupus erythematous); neurological disorders (e.g., epilepsy, stroke, fungal, parasitic, protozoan or helminthic infections; neurological disorders disease, dementia, or Parkinson's disease, dementia, or Parkinson's disease, dementia, or Parkinson's disease, independental disorders (e.g., achondroplastic dwarfism, Cushing's disease, hypothyroidism or hydrocephalus); endocrine disorders (e.g., achondroplastic dwarfism, Cushing's disease, hypothyroidism or hydrocephalus); endocrine disorders (e.g., cystic fibrosis or hypotholesterolesmia). The present sequence represents an INTSIG protein of the invention.

Sequence 414 AA;

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13;
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                                                                                                                                                                                                                               253
                                                                                                                                                                                                                                                                                                         354 AIKWDPIGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANL 413
                                                                                                                                                                                                                                                                                                                          TGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAK 301
                                                                                                                                                                                                                                                        QOFPFHSA--PALDVDWQSNNTFASCS---TDMCIHVCKL---GQDRPIKTFQGHTNEVN 353
                                                                                                                                                                                                                                                                              254 NILIGHCAEISSASFNW-----DCSLILTGSMDKTCKLWDATNGKCVATLTGHDDEIL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins AAR85851-92 are protein which contain at least one WD-40 (also called beta-transducing homologous) amino acid repeat motifs. The WD-40 regions are involved in protein-protein interactions between proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WD40 repeat region; beta-transducin; protein-protein interaction; drug; intracellular signalling; protein kinase C; homology; motif; modulator; receptors of activated protein kinase; enzyme activity; isozyme; human.
                                                                                                                                                                     | ::|| | ::|:| :| ::|::| DKIATGSFDKTCKLWSVETGK-----CYHTFR-----GHTAEIVCLSFNPQSTLVA
                                                                                                                                                                                                                    ---HAAAAAAAATNQQGSA-KNGE--
                                                                          LLTASRTEQVKLLIÓRLOEKLGÓNSNHTFYLFKVLKAHILPLTNVALNKSGSCFITGSYD
                                                                                                  ----NTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESBVFICAW-NPVS
                                                                                                                             --TLEGHRNVYAIAFNNPYG
                                                                                                                                                    DILIVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLA
                                                                                                                                                                                                                                                                                                                                                           MLASASFDSTVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIW 469

    which alter tinteracts with

                         85;
Length 414;
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity of a protein, eg. protein kinase C, which protein contg. a WD-40 region.
13.7%; Score 374.5; DB 6; 26.7%; Pred. No. 3.2e-26; ive 55; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WD-40 domain-contg. YCW2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 168-170; 351pp;
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              Similarity
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                      111;
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  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 PMHTLKGH------YNWVLCVSWSPDGEVIATGSMDNTIRLWDPKSGQCLGDALR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QHKGPIFALKWN-----KKGN--FILSAGVDKTTIIWDAHTGBAKQQFPFHSAPALDVDW 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DINSÓGRCINILKSHAHWVNHLSLSTDYALRIGAFDHTGKKFSTPBEAQKKALENYEKIC 364
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involved in intracellular signalling. An example of such an interaction is between protein kinase C and receptors of activated protein kinase (RACK), esp. RACK-1 (RAR85850). Proteins AAR85851-82 were isolated based on homology with beta-transducin, whereas proteins AAR85882-92 were isolated based on homology with the WD-40 consensus sequence (AAR85893). The proteins were used to construct the poptides AAR84928-R85063 and AAR85786-R85842. The peptides can be used to identify target proteins contg. WD-40 modifs, as modulators of enzyme esp. isozyme, activity of proteins involved in protein interaction and to screen for drugs that will affect protein interaction involving WD-40 domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FDGR----PIESLSLIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           13.7%; Score 374.5; DB 2; 23.6%; Pred. No. 4.5e-26; ive 85; Mismatches 167;
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Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----EGGQD----VPSNKDVTSLDW----N 234
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                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABL3072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AAATNOO-----GSAKNGENTAN----GEENGAHTIANNHTDMMEVDGD--VEIPSNKA
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                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 366.5; DB 4; Length 481;
llarity 27.5%; Pred. No. 2.3e-25;
Conservative 61; Mismatches 175; Indels 101;
                                                                                                                                                                                                Disclosure; SEQ ID NO 5250; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 IMVSASEDATIRIWDFETGEYERSLKGHTDSV------QDVA------FDAQGK 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 TGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIK 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 EVIEGAPIKNIKRIPGEW-------IPRPPEK-FSLIGHRASITRVIFHPIFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---YC-----VKTYTGHREWVRMVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 DEVNFLVYRYLQESGFSHSAFTFGIESHIS---QSNINGALVPPAALISIIQKGLQYVEA
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                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%; Score 365; DB 4; Length 411; 22.7%; Pred. No. 2.5e-25; ive 72; Mismatches 155; Indels 148;
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                                             Drosophila melanogaster polypeptide SEQ {
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m j} NO 13572.
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ABB62260 standard; protein; 411

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

August Run on:

9, 2004, 16:41:43; Search time 13.3333 Seconds (without alignments) 3708.183 Million cell updates/sec

US-09-987-701-2 2726 · I MSISSDEVNFLVYRYLQESG.....GDKVGASASDGSVCVLDLRK score:

Sequence:

514

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

78:* PIR Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

probable membrane protein YBR103w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YBR0832
C;Species: Saccharomyces cerevisian VBR0832
C;Species: Saccharomyces cerevisian 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S48268; S45971; S44683
R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
A;File: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Ricerence number: S48258; MUID:95208357; PMID:7900426
A;Accession: S48268
A;Accession: S48268

A,Molecule type: DNA
A,Residues: 1-535 <MAN>
A,Residues: 1-535 <MAN>
A,Residues: 1-535 <MAN>
A,Zross-references: EMBL:X78993; NID:g476045; PIDN:CAA55606.1; PID:g476059
R,Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A,Reference number: S45927

A;Accession: 845971
A;Molecule type: DNA
A;Rocessidues: 1535 <FE2>
A;Cross-references: EMBL:235972; MIPS:YBR103w
C;Genetics: A;Genetics: A

DB 2; Length 535;

15; 49 20 Gaps 1 MSISSDEVNFLVYRYLQESGFSHSA------FTFGIKSHISQSNINGALVPPAAL 97; Query Match
18.4%; Score 502.5; DB 2; Length!
Best Local Similarity 24.9%; Pred. No. 3.3e-28;
Matches 142; Conservative 100; Mismatches 232; Indels 셤 à

50 ISIIQKGLQYVEAEVSINEDG----TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ 106 ò

101 В 107 QAAAAAAAAAAAAQQGSAKWGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLR 166 102 SSEGRFTLETNSESNKAGEDGASTVERETQEDDTNSIDSSD--DLDGFVKI--LKEIV-ò g

167 GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTQ-----LVLRHCIREGG 219 $\stackrel{>}{\circ}$ g

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beta transducin-like protein - Podospora anserina
C;Species: Podospora anserina
C;Dacession: T18521
R;Saupe, S.; Turcq, B.; Begueret, J.
Gene 162, 135-139, 1995
A;Title: A gene responsible for vegetative incompatibility in the fungus Podospora anseri
A;Reference number: Z18944; MUD:96009891; PMID:7557402
                                                                                                                                                                                                                                                   C)Accession: A12155
R)Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Makazai, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A; Enference number: AB1807; MUID:21595285; PMID:11759840
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1258 cKUR>
A; Cross-references: GB:BA000019; PIDN:BAB74499.1; PID:G17131893; GSPDB:GN00179
A; Cross-references: ctrain PCC 7120
C; Genetics:
A; Gene: a1r2800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS 224
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A;Molecule type: DNA
A;Rossidues: 1-1356 cSAU>
A;Cross-references: EMBL:L28125; NID:g607002; PID:g607003; PIDN:AAA85775.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----CCTGRCVGI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1100 -----LRGHSNRVYSAIFSPNGEIIATGSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWOSNNTFASCSTDWCIHVCKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 QDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1258;
                                                                                                                                                           A12155
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp.
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 974 LECHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGOCFQILLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.0%; Score 463.5; DB 2;
31.8%; Pred. No. 6.7e-25;
iive 44; Mismatches 100;
                                                                 HINSVRSVAFSSDGLILASGSDDETIKLWDVK 1482
                                         -TGGIFEVCWNAAGDKVGASASDGSVCVLDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASGSFDKCVHIWNTQTGALVHSYR 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1074 GOLLASASADOSVRLWD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458
                                                                                  1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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402239
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC2239
C;Accession: AC2239
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Status: preliminary
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A;Residues: 1-1526 «KUR»
A;Cross-references: CB:BA000019; PIDN:BAB75165.1; PID:g17132599; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                                                                                                279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGN
                            QDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGN
                                                 SSGKTINQVICLAWSHDGNSIVIGVENGELRLWNKIGALLNVLNFHRAPIVSVKWNKDGT
                                                                                                      -HSAP---ALDVDWQSNNTFAS
                                                                                                                                                                                  325 CSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV
                                                                                                                                                                                                                                                            HDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEP
                                                                                                                                                                                                                                                                                    395 NSFYGHSQSIVSASWV------GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGAHTIANNHIDMMEVDGDVEIPPNKAV-VLRGHESEVFICAWNPVSDLLASGSGDSTAR
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29.8%; Pred. No. 6.8e-26;
tive 76; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                          445 VYSVAFSPDGRYLASGSFDKCVHIW-----NTQTGAL-
                                                                                                                                                                                                                                                                                                                                                                                                                     482 GTGGIFEVCWNAAGDKVGA--SASDGSVCVL 510
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNDYIFDLSWNCAGNKISVAYSLQEGSVVAI 535
                                                                                                        280 FILSAGVDKTTIIWDAHTGEAKQOFPF--
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Best Local Similarity 29.8%
Matches 117; Conservative
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                    :552 KTVKLMRSHDGHLLHTFSGHSNVVYSSSFSPDGRYTARASASEDKTVKIWQIDGHLLTTLPQ 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: AI2493
A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-1189 «KUR>
A;Cross-references: GB:BA000020; PIDN:BAB78213.1; PID:g17135667; GSPDB:GN00180
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                       421
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244 SYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ 302
                                                                                           .441 TLIGHDNEVNKVNFSPDGKTLASASRDNTVKLWNVSDGKFKKTLKGHTDEVFWVSFSPDG
                                                                                                                                                          806 CLDTLKKHTNRIWSVAFHPQGHLFVSGGDDHAAKIWBLGTGQCIKTFQGHSNATYIIAHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             925 GSADRIIKLWSPHTGQCLHTLHGHGSWVWAIAFSLD-----DKLLASGSYDHTVKI
                                                                                                                                     NLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFD
                                                                                                                                                                                                          STVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 GHESEVFICAWNPVSDLLASGSGDSTARIWNLSE----NSTSGSTQLVLRHCIREGGQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 -----DVPSNK----DVTSLDWNSEGTLLATGSYDGFARIW-TKDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 LASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDV--D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 WOSNNTFASCSTDMCIHVCKLG------QDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 WDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNIQIGALVHSYRGIGGI
                                                                  OFFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 439.5; DB 2; Length 29.0%; Pred. No. 3.2e-23; tive 65; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                     HOAGVMSAIFSPDGKTLISGSLD 1634
                                                                                                                                                                                                                                                                                 GTGGIFEVCWNAAGDKVGASASD 504
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Best Local Similarity
Matches 109; Conserva
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A;Genome: plasmid
                                                                  303
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WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: Ar2071
Nakazaki, N.; Nakmow, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S DA, Res. 8, 205-213, 2001
A;Ritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21592285; PMID:11759840
A;Accession: Ar2071
A;Status: preliminary
A;Accession: Ar2071
A;Status: Complete GB:BA000019; PIDN:BAB73823.1; PID:g17131215; GSPDB:GN00179
A;Accessimental source: strain PCC 7120
C;Genetics:
A;Gene: all2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAASGICIQILEGHGGWVHSVAFSPDGQRVASGSIDGIIKIWDAASGICIQILEGHGGWV 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1010 GSVWSVAFSPDGQRVASGSDDKTIKIWDTASGTCTQTLEGHGGWVQSVVFSPDGQRVASG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::::||
----EVLAGNSGVYAVSFLHDGSIIATA 1381
                                                                                       12;
                                                                                                                                                                                                                                                                                    309 APALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRGTGG-I 486
                                                                                                                                                                                                                ANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGD
                                                                                                                                                                                                                                                            STARIWNLSENSTSGS-TQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFA
                                                                                                                                                                                                                                                                                                                                 250 RIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVIRGHESEVFICAWNPVSDL
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                                                                                                                      78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAAASQQGSAKNGE-----NT
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                                                                                     70;
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                                                  ; DB 2; Length 1356; 1.3e-24;
                                                                                     Indels
                                                                                   73; Mismatches 178;
                                                  16.9%; Score 460; 27.9%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :: | : : | : : | OSVAFSPDGQRVASGSSDKTIKIWD 1205
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                                                                                     Conservative
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Best Local Similarity
Matches 109; Conserv
                                                                    Similarity
A;Gene: het-e1
A;Introns: 761/3
                                                                      Best Local Sim
Matches 124;
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                                                                                                                                                                                                                     16.0%;
30.8%;
                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.8%
Matches 119; Conservative
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NA, Fater C. Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A, Reference number: AB1807; MUID:21595285; PMID:11759840

A, Reternce number: AB1800

A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-1227

A, Molecule type: DNA
A, Residues: 1-1227

A, Status: preliminary
A, Status: Stalininary
A, Status: Stalininary
A, Status: Stalininary
A, Status: Stalininary
A, Gross-references: GB:BA000019; PIDN:BAB77553.1; PID:g17135007; GSPDB:GN00179
A, Gross-references: Strain PCC 7120
C, Genetics:
A, Gene: alr0029
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AE1866
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE1866
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                 ABSULT 7
AB1810.

AB1810.

AB1810.

AB1810.

C,Species: Nostcc sp. PCC 7120

A;Note: Nostcc sp. strain PCC 7120

A;Note: Nostcc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AB1810

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      862 WAIAFSPDGRTLISCSDDQTARLWDVITGNSLNILRGYTRDVYSVAFSPDSQILASGRDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 VDGDVEI----PPNKAV-VLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSE----NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         682 LSKNTNKVYSVAFSPDGRILASASQDQTIKLWDIATGNCQQTLIGHDDWVWSVTFSPVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRPLLLASSSADQHIKLWDVATGKCLKTLKGHTREVHSVSFSPDGQTLASSGEDSTVRLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.1%; Score 439; DB 2; Length 1227; 25.4%; Pred. No. 3.7e-23; ive 83; Mismatches 157; Indels 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP-
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----WEADSNRVWAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Matches 122;
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S. Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A; Title: S. Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: AE1866
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-1708 «XUR>
A;Cross-references: GB:BA000019; PIDN:BAB72436.1; PID:g17129823; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1322 NGETIGSASI------DATLKLWSPQGLLLGTLKGHNSWVNSVSFSPDGRIFASGS 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 ARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW 427
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A;Status: prelimitary
A;Rolecule type: DNA
A;Residues: 1-1711 <KUR>
A;Coss-references: GB:BA000019; PIDN:BAB77808.1; PID:g17135262; GSPDB:GN00179
A;Genetics: ctrain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVIRGHESEVFICAWNPV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNIQTGALVHSYRG-TGGI 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 GDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1372 RDKTVTLWRWDE-----VLLRNPKGDG-----NDWVTSISFSSDGETLAAASRDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDDTTVKLWS-RDGQLLHTLKEHSRRVNGVAWSPDGQ-----ILASASIDGTVKLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGEENGAHTIANNHTDMMEVDGDVEIPPNKAVV---LRGHESEVFICAWNPVSDLLASGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 APALDVDWQSNN-TFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.2%; Score 414; DB 2; Length 1711; Best Local Similarity 25.5%; Pred. No. 3.6e-21; Matches 126; Conservative 74; Mismatches 178; Indels 116; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                       Length 1708;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                   ; Score 437; DB 2; L6; Pred. No. 8.1e-23; 69; Mismatches 154;
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qa	1281 DGQTIVSAGADNTVKLWSRNGTLLTTLBGHNEAVWQVIFSPD 1322	Db 419 pdsof.Lapasumptiviti werest.Lift.Echtokivist treedicol.Lapasumptiviti werest.
b oy	181 SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLL 240	295 AHTGEAKQOPPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT 34
ž q	241 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKMNKKGNFILSAGVDKTTIIWDA 295	Db 479 L-DGKELRTFRGHQDMIWSVSFSPDGKQIATASGDRTVKLWSL-DGKELQTLRGHQ 532 Qy 350 NEVNAIKWDPTGNLLASGSDDWTLKIWSMKQDNCVHDLQCHNKEIYTIKWSPTGPG 405
λ ζ 90	296	Db 533 NGVNSVTFSPDGKLIATASGDRTVKLMNSKGQE-LETLYGHTDAVNSVAFSPDGTSIATA 591 Qy 406TNNPNANIMASASFDSTVRLWDVDRGICI 435
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	3	Db 592 GNDKTAKIWKLNSPNSIIVRGHEDEVFDLVFSPNGKYIATAKAKIAKIVGHKLQEL 651 Qy 436 HTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAA 494
દે વ	F X	652 RİFNGHQƏRVNKLS 495 GDKVGASASDGSV : : :
& 90	440 KHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGIFBVCWNAAGDKV 498	Db 711 GQLIATASEDKTV 723 RESULT 11
, Ag q	499 GASASDGSVCVLDL 512 1656 ASGGHDTTVKVWNL 1669] - Nostoc sp. (strain PCC 7120) 7120 is a synonym of Anabaena sp.
E 0		:-2002 inabe, A suda, M.
ND-40 re C;Specie A;Note: C;Date:	D-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120) ;Species: Nostoc sp. PCC 7120 ;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 ;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002	tence of the Filamentous Nitrogen-fixing Cyanobac JID:21595285, PMID:11759840
7, Acces 7, Kanek Nakaza) NA Res N, Title:	Jk, C.P.; Kuritz, T.; Sasar gimoto, M.; Takazawa, M.; Y. Lence of the Filamentous Nii JID:21595285; PMID:11759840	A;Status: preliminary A;Molecule type: DNA A;Mosidues: 1-1747 < KUR> A;Cross-references: GB-BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179 A;Experimental source: strain PCC 7120
A, Acces A, Statui A, Molecu A, Residu A, Cross-	one: ActBBs; : preliminary le type: DNA seil-1-34 KURP. references: GB:BA000019; PIDN:BAB72622.1; PID:q17130010; GSPDB:GN00179	A;Gene: all0283 Query Match Best Local Similarity 15.1%; Score 411.5; DB 2; Length 1747; Best Local Similarity 27.4%; Pred. No. 5.5e-21; Matches 114; Conservative 67; Mismatches 156; Indels 79; Gans 10;
A,Experi C,Geneti A,Gene:	mental source: strain PCC 7120 Cs: al10664	165 LRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQ
Query Ma Best Loc Matches	uery Match 15.1%; Score 412.5; DB 2; Length 934; est Local Similarity 23.7%; Pred. No. 2e-21; atches 131; Conservative 113; Mismatches 196; Indels 113; Gaps 21;	OY 209 LVLRHCIREGGODVBSNK
<u>۲</u> و	8 VNFLVYRVLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYVBAEVSIN 67 ::	227DVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKANKKG
\$ q	68 EDGTLFDGRPIESLSLIDA-VMPDVVQTRQQAYRDKLAQQQAAAAAAAA 118 	1430 SQKSNVNSVSFNPDGKTFASAGWDGNITIWQRE-TLAHSSLSTIQKNQNIITTVSYSPDG 279 NFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQ-SNNTPASCSTDMCIHVCKLG
દ્ર વ	119 SQQSSAKNGENTANGEBNGAHTIANNHTDMMEVDGDVEIPPNKAVVLRCHESEVF-ICAW 177	1489 338
<i>ኢ</i> ብ	178 NPVSDLLASGSGDSTARIMNLSENSTSGSTQLVLRHCIREGGQDVPSNKD-VTSLDWN 234	1549 DGQLLRTLTGHND 398 KWSPTGPGTNNPN :
à	235 SEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWD 294	Db 1608 KFSPDSHTLASASWDNTIKLWQVTDGKLINNLNGHIDGVTSLSFSPDGBIL 1658

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A;Experimental source: strain 972h-; cosmid c1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 VYNSSPV----TEITEIKQVTFTGGEDIKSDFFKVIPTKHPVTCADWRPLLQENYHVYE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 SGSGDSTARIWNLS----ENSTSGSTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 DPTGNILASCSDDMTLKIWSMKQD---NCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLM 414
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                                                                                                                                                                                                                                      WD repeat protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: T40883
R;Wood, V, Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
Submitted to the BMBL Data Library, September 1998
A;Reference number: Z21954
A;Reference number: Z21954
A;Reference preliminary; translated from GB/BMBL/DDBJ
A;Rocue; preliminary; translated from GB/BMBL/DDBJ
A;Residues: 1-564 <WOO>
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   ASGSFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 390.5; DB 2;
llarity 24.5%; Pred. No. 3.7e-20;
Conservative 107; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 18/1; 273/3; 413/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: SPDB:SPCC1235.09
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Best Local Similarity
Matches 133; Conserv
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876086 beta transducin-like protein, 190K - Synechocystis sp. (strain PCC 6803)

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A;Cross-references: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10064.1; PID:d1010711; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A;Superfamily: unassigned WD repeat proteins; WD repeat homology
F;1051-1084;Domain: WD repeat homology <WD01>
F;1092-1125;Domain: WD repeat homology <WD01>
                                                                                                            R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2195
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 GGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 RDKLAQQQAAAAAAAAASQQGSAKNGENTANGE--ENGAHTIANNHTDMMEVDGDVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1362 RDKTARLWTTEGECVAVLADHQGWVREGQFSPDGQWIVTGS---ADKTAQLWNVLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 PPNKAVVLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1415 ---KKLTVLRGHQDAVLNVRFSPDSQXIVTASKDGTARVWN-----NTGRELAVLRH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 QDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1693;
                                                                                                                                                                                                                                                                                                   Status: nucleic acid sequence not shown; translation not shown; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                  A; Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.3%; Score 388.5; DB 2;
Best Local Similarity 28.5%; Pred. No. 2.3e-19;
Matches 107; Conservative 52; Mismatches 138;
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F;1584-1617/Domain:
F;1625-1658/Domain:
                                                                                  C, Accession: S76086
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F;1174-1207/Domain:
F;1256-1289/Domain:
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DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A,Feference number: AB107; MUID:21595285, PMID:11759840
A,Accession: AH2195
A,Molecule: Preliminary
A,Molecule: 1-756 «KUR»
A,Molecule: 1-756 «KUR»
A,Cross-references: GB:BA000019, PIDN:BAB74818.1; PID:g17132214; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: alr3119
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                                                                                                                                                                                                                                                                                                                                                                                                                              274 VKVLNKLLETDIQRRYQSADEVMNDLIKQRSLLSRLKTTIPKSAIFSRSWSASTSLTAST 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 TKKQAWKLLNGRLK-QQLLINTMSALLGLVGVGHLQSLPQLITKFSEISTQP---YTLKG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGDDVPSNKD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTTIIWDAHTGEAKQQFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQ 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGT 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SDSQTLASGSKDKTIKLWNLSTGKTIRTLRGHSDKVNSVAYVPRDSTVLASGSNDNT 625
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                             119;
                                                                                                                                                                                                                                    14.0%; Score 382.5; DB 2; Length 676; 23.6%; Pred. No. 1.8e-19;
                                                                                                                                                                                                                                                                                                                  21 FSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYVEA----
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Matches 123; Conserv
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-----ATGSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKGNF 280

1053 AGDDHTARLWSFSGQQLVQFPGHQGTVWCISFSPDGKHIATAADDRIVRLWNLKGKLLVR 1112

993 HEDIIWSANFSPDGKYIATASSDRTARLWNFSGQQLAKFQGHQGYVRSVSFSPDGKHIAT 1052

HESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTS-----GSTQLVL-----RHCIR 216

168

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954 AWVRSVSFSRDGQYILIASDDCTAR------LWNLQG------KQLISLQG 992

108 AAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVIRG 167

903 ALMSAMRSG----KALQALVKDGRSLAKYPATSPLLALQTILDNIQERNQ-----FQGHQ

g ò

48 ALISIIQKGLQYVEAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQ 107

94; Mismatches 193; Indels 130;

Score 382; DB 2; Pred. No. 6.1e-19;

14.0%; 22.6%;

Conservative

al Similarity 122; Conserv

Query Match Best Local S: Matches 122

RPIKTFOGHTNEVNAIKWDPIGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKW 399

O-FSAFQGHQSTVRSVDFSPDGQKVVTAADDRTVRLWNIKGEELLQFL-GHRGKVWSVSF

SPIGPGINNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLAS

ILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTF-ASCSTDMCIHVCKLGQD 339

281

241

340 1232 400

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RESULT 15
AB2410
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. strain PCC 7120
C; Species: Nostoc sp. strain PCC 7120
C; Accession: AB2410
C; Accession: AB1807; WID:2159285; PMID:11759840
A; Reference number: AB1807; WID:21595285; PMID:11759840
A; Accession: AB2410
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Genetics

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9, 2004, 16:48:48
completed: August
 Search cor
Job time
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1340 ASSDLTTRLWSLDGQELMQFKGHDKWVRYVSFSCNGQHIATAADDCTARLWNLAGRQVG 1398

460 GSFDKCVHIWNTQTGALV-----

-----HSYRGIGGIFEVCWNAAGDKVG 499

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August 9, 2004, 16:41:13; Search time 34.6667 Seconds (without alignments) 4678.164 Million cell updates/sec
                                                                                                                                                                                         2726
1 MSISSDEVNFLVYRYLQESG......GDKVGASASDGSVCVLDLRK 514
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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sp_vertebrate:*
sp_unclassified:*
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Perfect score:
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                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                            Searched:
                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O8bhi5 mus musculu	mus	mus			Sing	O86uv2 homo sapien	OSCOAL MUS MUSCULU	O9xxk1 drosophila	O9fn19 arabidopsis	OBved3 mus musculu	O95ri9 drosophila	O8x1p4 podospora a			Q8x1p2 podospora a
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SUMMARIES	ID	Q8BHJ5	Q8CBG4	Q9EQD4	O7SZM9	OBBYO4	OBBMMO	QB6UY2	OBCOAL	O9XZK1	Q9FN19	Q8VEG3	Q95RJ9	O8X1P4	08X1P5	O8X1P3	Q8X1P2
	DB	11	11	11	13	11	11	4	11	Ŋ	10	11	2	m	m	m	m
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ф	Query	98.7	98.6	98.6	97.0	91.1	91.0	89.4	72.4	69.8	50.9	40.2	33.9	17.5	17.4	17.3	16.5
	Score	2691	. 2688	2687	2644.5	2484.5	2480.5	2437	1972.5	1904.5	1387	1096	923.5	477	474	472	449
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Q8YL09	Q8Z0R1	Q8YZI2	Q8Z019	Q8YZ23	Q8Z020	074845	QBYSG6	Q8YMU3	Q8N136	Q8TMX4	074855	Q9VPR4	Q8T4A2	Q8N776	09D4T2	082054	QBYTD1	869960	Q9XBD8	096995	Q803D2	093531	Q7ZXK9	Q8YZ16	080990	098HK1	Q90ZL4	Q9DCZ7
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16.1	16.1	16.0	15.2	15.1	15.1	14.3	14.0	14.0	13.8	13.6	13.6	13.6	13.6	13.6	13.5	13.5	13.5	13.5	13.4	13.3	13.3	13.2	13.2	13.2		13.2	•	13.0
439.5	439	437	414	412.5	411.5	390.5	382.5	382	376	372	371.5	370.5	370.5	370	368.5	368.5	368.5	368	364	362.5	യ	361	361	360	359	358.5		354
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ALIGNMENTS

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us-09-987-701-2.rspt

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STRAIN=CSTEL/61; TISSUE=Cerebellum,

MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

The FANTOM Consortium,

The RAKEN Genome Exploration Research Group Phase I & II Team;

A nalysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

In Nature 420:563-573(2002)

R BMEL, AK036064; BAC29294.1; -..

R BMEL, AK036064; BAC29294.1; -..

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                                                                                                                                                                                         1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
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                                                                                                     Indels 0; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae; Mus
         98.7%; Score 2691; DB 11; Length 514; 98.6%; Pred. No. 6.2e-179; ive 2; Mismatches 5; Indels 0
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Query Match
Best Local Similarity 98.69
Matches 507; Conservative
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Zhang X., Dormady S., Basch R.;
Zhang X., Dormady S., Basch R.;
"Identification of four human cDNAs that are differentially expressed
"Identification of four human cDNAs that are differentially expressed
Bub Submitted (MAY-2000) to the BMBL/GenBank/DDBJ databases.
BMBL, AF268195; AAG44738.1;
InterPro; IPR006594; LisH.
InterPro; IPR001669; WD40.
PFEMP; PR00400; WD40.
PFEMP; PR00400; WD40.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
                                                                                                                                                                                                                                  98.6%; Score 2688; DB 11; Length 514; 98.4%; Pred. No. 1e-178; trive 3; Mismatches 5; Indels 0;
PROSITE; PS50896; LISH; 1.
PROSITE; PS0678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
SEQUENCE 514 AA; 55689 MW; 133ED3753A725029 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 98.4%
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"Fushin Protein of Retinoic Acid Receptor (alpha) with Promyelocytic
Leukemia Protein or Promyelocytic Leukemia Zinc Finger Protein
Recruits N-CoR-TBLRI Corepressor Complex to Repress Transcription in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor co-repressor complex subunit TBLR1.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                            ;
0
                                                                                                                                   514;
                                                                                                                             Query Match

98.6%; Score 2687; DB 11; Length
Best Local Similarity 98.4%; Pred. No. 1.2e-178;
Matches 506; Conservative 2; Mismatches 6; Indels
                                                                                                      514 AA; 55689 MW; 6A72CE68A40C141F CRC64;
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            SMART; SM00667; Lish; I.
SMART; SM00320; WD40; 8.
PROSITE; PS50896; LISH; I.
PROSITE; PS00679; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50082; WD REPEATS 2; 6.
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PD000018; WD40; 3.
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                                                                                         Repeat; WD repeat.
SEQUENCE 514 AA;
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61 EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQTAAAAAAAAA 120
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The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thailysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 KWDPTGNLLASCSDDMTLKIWSMKHDTCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLML
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SEQUENCE FROM N.A.
STAIN-CSTBL/6; TISSUE=Brain;
MEDLINE=22388257; Pubmed=12477932;
StrausBerg R.L., Felngold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                              519;
                                                                                                                                                                               'n
                                                                                                           DB 13; Length
                                                                                                                                       1.1e-175;
thes 10; Indels
                                   5E998EDC8C892296 CRC64;
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Last annotation update)
                                                                                                    Score 2644.5;
Pred. No. 1.1e-4; Mismatches
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                                   519 AA; 56043 MW;
                                                                                                    97.0%;
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                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 500; Conserv
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Q8BYQ4;
01-MAR-2003 (
Receptor.
SEQUENCE
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DKTTIIWDAHTGBAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQ 346
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Pituitary;
STRAIN=22334683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,700 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK030547; BAC27015.1;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 527;
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                                                                                             467 HIWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK
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87.7%; Pred. No. 2.8e-164;
Live 28; Mismatches 22; Indels
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ProDom; PD000018; WD40; 3.
BYART; SM00567; Lis8; 1.
SWART; SM00520; WD40; 8.
PROSITE; PS500896; LISH; 1.
PROSITE; PS50081; WD_REPEATS 1; 4.
PROSITE; PS50084; WD_REPEATS 2; 6.
PROSITE; PS50084; WD_REPEATS_2 6.
PROSITE; PS50084; WD_REPEATS_REGION; 1.
SEQUENCE 527 AA; 56832 MM; 0466F764ABA25CB0 CRC64;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                     Created)
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MGD; MGI:1336172; Tbllx.
InterPro; IPR006594; LisH.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 87.7%;
Matches 463; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Rh Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rh Eromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robar S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Gones S.J., Marra M.A.,
T. "Generation and initial malysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.;
Submitrd (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK036674; BAC30092.1; -.
EMBL; BC043105; AAH43105.1; -.
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PROSITE; PS00878; WD_REPEATS 1; 4.
PROSITE; PS50082; WD_REPEATS 2; 4.
PROSITE; PS50294; WD_REPEATS REGION; 1.
SEQUENCE 527 AA; 56802 NW; 146435A9C51DFDA6 CRC64;
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MGD; MG1:1336172; Tbl1x.

InterPro; IPR006594; LisH.

InterPro; IPR001680; WD40.

PEam; PF00400; WD40; 8.

PRINTS; PR00320; GPROTBINBRPT.

ProDom; PD000018; WD40; 3.

SMART; SM00667; LisH; 1.

SMART; SM00320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
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Matches 464; Conservative
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01-OCT-2003 (
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Altschul S.P., Zeeberg B.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

A phykins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B rownstein M.J., Usdin T.B., Tooshiyuki S., Casavant T.L., Scheetz T.E.,

B sake S.A., McEwan P.J., McKernan K.J., Marason R.D., Mullahy S.J.,

B Richards S., Morley K.C., Hale S., Garcia A.E., Gunsarene P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.E., Gubbs R.A.,

Pahey J., Helton B.K., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

Redersation and initial analysis of more than 15,000 full-length human
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                                               GHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGT
                                                                                                                    NNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCV
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                                                                                                                                                                                                                                 514
                                                                                                                                                                                                                                                          480 HIWNIQSGSLVHSYRGTGGIFEVCWNARGDKVGASASDGSVCVLDLRK 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human),
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Strausberg R.,
Strausberg R.,
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO52304; AAH52304.1; -
InterPro; IPR006594; LisH.
InterPro; IPR001680; WD40.
Pfan, PP00400; WD40; 8.
PRINTS; PR00320; GPROTINBRPT.
ProDom; PD000018; WD40; 3.
SWART; SW00667; LisH; 1.
SWART; SW00667; LisH; 1.
PROSITE; PS50896; LISH; 1.
PROSITE; PS50896; WD REPEATS 1; 4.
PROSITE; PS50892; WD REPEATS 2; 6.
PROSITE; PS50892; WD REPEATS 2; 6.
PROSITE; PS50892; WD REPEATS 2; 6.
PROSITE; PS50894; WD REPEATS 2; 6.
PROSITE; PS50894; WD REPEATS REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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86.0%; Pred. No. 3.4e-161;
ive 33; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Simi
Matches 453;
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C STRAIN=CSTBL/67 ITSSUE=Medulla oblongata;

X MEDLINE=22354683; PubMed=12466851;

A The FANTON Consortium,

A the RANTON Consortium,

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

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B the RIKEN Genome Exploration Research Group Phase I & II Team;

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDINE=20196006; PubMed=10731132;

MEDINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeiffer B.D.,

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Burtis K.C. Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pluikov B.C.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

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Kalmael B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liang Y., Lin X.,
                                                                                     104 AQQQAAAAAAAAAAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAV 163
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                                                                                                                            3 AATATSTAATTPAAAAQQNPPKNGEATVNGEENGAHAI-NNHSKPMEIDGDVEIPPSKAT 61
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DB 11; Length 412;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                              28; Indels
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Last annotation update)
72.4%; Score 1972.5; DB 11
87.6%; Pred. No. 4.4e-129;
ive 22; Mismatches 28;
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                                                Matches 360; Conservative
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A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy D., Mishon D.L.,
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J. Yellong F.M., Zhong W., Zhon M., Zhang G., Zhao Q., Xao
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
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CHOWCEN L. A. Furmmatti S.R., Karra K., Kearney L., Kim S.H., Lee B.,
CHOWCEN K.A., Hummatti S.R., Karra K., Kearney L., Kim S.H., Lee B.,
LOMOCEN M.A., Max J., Maxda P., Moshrefi A.R., Moshrefi M., Nixon K.,
CHOWCEN M.A., Max J., Pefaifer B., Punch E., Snir E., Twomey B.,
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99234084; PubMed=10215623;
Dong X., Tsuda L., Zavitz K.H., Lin M., li S., Carthew R.W.,
Zipursky S.L.;
"ebi regulates epidermal growth factor receptor signaling pathways in
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Best Local Similarity 54.8%; Pred. No. 4.9e-124;
Matches 385; Conservative 51; Mismatches 75; Indels 191; Gaps
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SWART; SM00667; LiseH; 1.

SWOSITE; PS50896; LISH; 1.

PROSITE; PS00037; WWB_l; 1.

PROSITE; PS00078; WD_REPEATS_1; 3.

PROSITE; PS50082; WD_REPEATS_2; 6.

PROSITE; PS50294; WD_REPEATS_2; 6.
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       AGGNQASTGGSNSTSTPAGGDLAAPGASQKKSQNSNEAGSSSSGNAGNANATSTDDAASS
                                        -- MEVDGDVEI PPNKAVVLRGHESEV
                                                                                                              FICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                          WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII
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                                                                                                                                                                                                WDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV
                                                                                                                                                                                                                    478 WDASTGQCTQQFAFHSAPALDVDWQTNQAFASCSTDQRIHVCRLGVNEPIKTFKGHTNEV
                                                                                                                                                                                                                                          NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNAN
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01-MAR-2001 (TrEWBLrel. 16, Last sequence update)
01-MAR-2003 (TrEWBLrel. 15, Last annotation update)
Genomic DNA, chromosome 5, TAC clone: KBK14 (ATBG67320/KBK14_4).
Arabidopsis thaliana (Mouse-ear cress).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Supermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";

DNA Res. 4:401-414(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka I. Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamada Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                                                                                                       "Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                           H.C.,
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Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chann M., , Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Narusaka M., Palin C.J., Quach H.L., Sakurai T., Satcou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.9%; Score 1387; DB 10; Length 613; 44.2%; Pred. No. 4.1e-88;
                                                                                                                                                                                                                                                                                                                                     | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Comparison | Com
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SEQUENCE 613 AA; 69772 MW; 04F40772311C0E76 CRC64;
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les 272; Conserv
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us-09-987-701-2.rspt

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EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRQ-----
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      524 AA; 52529 MW; 6C3D86110BA18D65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---NG--------AHTIANNHTDM-----
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*4.
                                                      EMBL, AV061286, AAL28841.1;

FlyBase; FBGN0023444; ebi.

GO; GO:00000074; P:regulation of cell cycle; IMP.

InterPro; IPR001005; Myb DNA_binding.

InterPro; IPR001069; Myd0.

FRam; PF00000, WD40.

PRINTS; FR00320; GPROTEINBRPT.

ProDom; PD000019; WD40; 1.

SMART; SM00320; Myd0: 3.

PROSITE; PS50896; LISH; 1.

PROSITE; PS50896; LISH; 1.

PROSITE; PS50896; Myd0: 3.

PROSITE; PS50896; WD REPEATS. 1; 2.

PROSITE; PS50898; WD REPEATS. 1; 2.

PROSITE; PS50898; WD REPEATS. 1; 2.

PROSITE; PS50898; WD REPEATS. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
33.9%; Score 923.5; DB 5;
Best Local Similarity 40.5%; Pred. No. 5.8e-56;
Matches 218; Conservative 39; Mismatches 64;
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Q8X1P4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 KIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNIQTGALVHSYRGIGGIFEVCWNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
Stapheton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapheton M., Chavez C., Dorsett V., Farfan D., Frise B., George R.
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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BBI OR CG403n.

Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha; Ephydroida; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 201;
                                                                                                                                                                                                                                                                                                                              Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018812; AAH18812.1;
InterPro; IPRO010680; WD40.
Pfam; PF00400; WD40;
PFAm; PF00400; WD40; 4.
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
SNART; SM00320; WD40; 4.
PROSITE; PS00678; WD REPEATS 1; 2.
PROSITE; PS00678; WD REPEATS 2; 3.
PROSITE; PS0082; WD_REPEATS 2; 3.
PROSITE; PS0982; WD_REPEATS 2; 3.
PROSITE; PS0983; WD_REPEATS 2; 3.
PROSITE; PS0983; WD_REPEATS 3; 3.
PROSITE; PS0983; WD_REPEATS 3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
201 AA; 22038 MW; 6B945F137B491818 CRC64;
                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to IRAl protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
40.2%; Score 1096; DB 11;
Best Local Similarity 99.0%; Pred. No. 1.5e-68;
Matches 199; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 AA
                                                                                                         201 AA
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
            AACFADNSVCVLDFR
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233 WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII 292
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Beta transducin-like protein HET-E2C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 -TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484
                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AAAAAAAAAAASQQGS-----AKNGENTANGEENGA----HTIANNHTDMMEVDG---D
                                                                                                                                                                                                                                                                                                                                                                                                                                                  829 EWNACTQTLEGHGSSVLSVAFSPDGQRVASGSDDKTIKIWDTASGTGTQTLEGHGGSVWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 VEIPP-----NKAV-----VIRGHESEVFICAWNPVSDLLASGSGDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             889 VAFSPDGQRVASGSDDKTIKIMDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 ASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASPDSTV
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                                                                                                                                                                                                                                                                                                                                                                              49 LISIIQKGLQYVEAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQA
                                                ESPAGENCE FROM N.A.

ESPAGENCE FROM N.A.

ESPAGENCE B., Balhadere P., Begueret J., Turcq B.;

"A new family of WD40 proteins implicated in vegetative
incompatibility, evidence for a major role of WD40 repeat domain in
the specificity of het-e and het-d genes.";

Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF32583; AAL37299.1;

InterPro; IPR007111; NACHT_NTPase.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                            17.5%; Score 477; DB 3; Length 1356; 26.2%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                   1356 AA; 149702 MW; 33148AF4A7B82826 CRC64;
                                                                                                                                                                                                                                                                                                                                                    86; Mismatches
                                                                                                                                                               Pfam; PF05729; NACHT; 1.
Pfam; PF05400; WD40; 10.
PRINTS; PR00320; QBROTEINBEPT.
Problom; PD000018; WD40; 10.
SWART; SM00320; WD40; 10.
PR0SITE; PS06081; NACHT; 1.
PROSITE; PS06078; WD REBEATS 1; 10.
PROSITE; PS50082; WD REBEATS 1; 10.
PROSITE; PS50082; WD REBEATS 2; 10.
PROSITE; PS50082; WD REPEATS 2; 10.
PROSITE; PS50082; WD REPEATS 2; 10.
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                                                                                                                                                                                                                                                                                                                                                      Conservative
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SEQUENCE 1356 AA
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Matches 133;
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Last sequence update) Last annotation update)

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(TrEMBLrel. 20, (TrEMBLrel. 20, TremBLrel. 25,

01-MAR-2002 01-MAR-2002 01-OCT-2003

Q8X1P5 Q8X1P5

08X1P5 ID 08 AC 08 DT 01 DT 01

PRELIMINARY;

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                                                                                                                                                                                                                                                              Espagne E., Balhadere P., Begueret J., Turcq B.;
"A new family of Wh00 proteins implicated in vegetative incompatibility; evidence for a major role of WD40 repeat domain in the specificity of het-e and het-d genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1232881, AAL37298.1;
InterPro; IPR0011; NACHT_NTPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 474; DB 3; Length 139; Pred. No. 4e-24; 86; Mismatches 222; Indels
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Pfan, PPG5729; NACH7, 1.
Pfan, PPG0400; WD40; 1.
PRINTS; PR00320; GPROTEINBRPT.
PROSIT; SM00320; WA40; 10.
PROSITS; PS5083; NACH7, 1.
PROSITS; PS5082; WD_REPEATS_1; 10.
PROSITS; PS5082; WD_REPEATS_2; 10.
PROSITS; PS5024; WD_REPEATS_3; 10.
PS5024; PS5024; WD_REPEATS_3; 10.
PS5024; PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
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PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_REPEATS_3; 10.
PS5024; WD_R
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Matches 132; Conservative
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=5145,
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Q8X1P3;
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Q8X1P3
ID Q8X1P:
AC Q8X1P:
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969 --SVWSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQTLEGHGNSVWSVAFSPDGQRVAS 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1027 GSDDKTIKIWDTASGTCTQTLEGHGGWVMSVAFSPDGQRVASGSIDGTIKIWDAASGTCT 1086
                                                                                                                                                                                                                                                                                                                                                                                                                         921 LEGHGSSVLSVAFSFDGQRVASGSGDKTIKIW---DTASGTGTQTLEGH----GG----- 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 AGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343 KTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPT 402
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                                                                                                                         165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 NKDVTSLDWNSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILS
                                                                                                                                                                                                                                                                                                                                                                                    26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 DKCVHIWNTQTGALVHSYRGTGG-IFEVCWNAAGDKVGASASDGSVCVLD 511
                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                               Length 1356;
                                                                                                                                                                                                                                                                                                                                                             17.3%; Score 472; DB 3; Length 13
31.7%; Pred. No. 5.5e-24;
ive 59; Mismatches 154; Indels
01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*40.
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Best Local Similarity 31.7%
Matches 111; Conservative
                                                            Podospora anserina
                                                                                                                  SEQUENCE FROM N.A.
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Search completed: August 9, 2004, 16:47:57 Job time : 37.6667 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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9, 2004, 16:39:47 ; Search time 48 Seconds (without alignments) 3025.613 Million cell updates/sec OM protein - protein search, using sw model August Run on:

US-09-987-701-4 Title: Perfect

2718 1 MSISSDEVNFLVYRYLQESG..........LPHHLVVIPLVALIELLVLK 514 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genescq11980s:* genescq12000s:* genescq12001s:* genescq12001s:* genescq12001s:* genescq12003bs:* genescq12003bs:* 29Jan04:* A Geneseq 1 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

+[::048		* 5				
. '	Score	Match	Length	DB		Description
١.	2488	91.5		4.	ı N	Aab95225 Human pro
ċ.	48			9	ABO07190	7190 Human
m	N	ď	S	7	S	Н
T	2132	ω.	S	'n	ABP41760	0
ıΩ	4	'n	39	ហ	ABP51424	4
G	721.	m	58	4	ABG21351	1 Novel
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ന	13	ä	20	4	AA004385	5
6	ч	0	16	4	ABG21350	21350 Novel
0	469	7	53	9	ABR52980	Abr52980 Protein s
_	4.	ë.	41	9	ADA13321	ĭ
N	70.	m	41	4		0
m	67.	m m	48	4	œ	Amino
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	366.5	13.5		4	AAB92844	
เก	.99	т М	48	Ŋ	ABB97306	Novel
7	Ŋ	ო	48	4	AAB68282	
œ	S	'n	35	m	AAG14893	1893
σ	Ŋ	m.	35	٣	AAG48119	3119
0	S	ω,	35	۲	ADB95040	Adb95040 A. thalia
_	S		34	m	AAG48120	3120
01	5	ش	34	w	AAG14894	1894
_	٠		40	۲.	ADE54235	235 Human Pr
	350	ď	33	~	AAW55957	395
ı۸	S		33	7	AAW58888	Aaw58888 Human lip

Ade59693 Human Pro	Ade59/05 Human Fro	9709 Human	Ade83378 Human Pro	Ade59701 Human Pro	Ade59713 Human Pro	Ade57861 Human Pro	Aar70002 OPDE 45 k	Ade58488 Rat Prote	Ade83492 Rat Prote	Ade54233 Rat Prote	Aar70005 OPDE 45 k	Abb59486 Drosophil	Aay79678 Drosophil	ın	Aaw25018 TATA-bind	Aar85868 WD-40 dom	Abb99407 Amino aci	Ada21145 Human sec
																	-	
ADE59693	ADE59697	ADE59709	ADE83378	ADE59701	ADE59713	ADE57861	AAR70002	ADE58488	ADE83492	ADE54233	AAR70005	ABB59486	AAY79678	AAW06085	AAW25018	AAR85868	ABB99407	ADA21145
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LO 1	350	S		350	350	350		349.5	349.5	349.5	349.5	342	341.5	339	339	338	338	338
	7 8 7			31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                             Human protein sequence SEQ ID NO:17352.
     AAB95225 standard; protein; 514 AA
                                                                                                                          29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-NAXY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                               28-JUL-2000; 2000EP-00116126.
                               (first entry)
                                                                        Homo sapiens.
                                                                                    EP1074617-A2.
                                26-JUN-2001
                                                                                                  07-FEB-2001.
                  AAB95225;
AAB95225
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(HELI-) HELIX RES INST.

Isogai T, Nishikawa T, Sugiyama T, Wakamatsu Ota T, Is Ishii S,

Primer sets for synthesizing polynucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length Saito K, Ya , Otsuki T; Hayashi K, S A, Nagai K, WPI; 2001-318749/34.

Yamamoto J;

Claim 8; SEQ ID NO 17352; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

12-DEC-2002

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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the the soligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13613 to AAH13613 to AAH13613 to AAH13613 represent human amino acid sequences, and AAH13629 to AAH13612 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 514 AA;
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                                                                              EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAASQ
                                                                                                                                                         61 BABVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAASQ
                                                                                                                                                                                        OGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPV
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                                                                                                                                                                                                           ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                                                                                                                                                                                                                                                                                            301 KOOFPFHSAPALDVDWOSNNTFASCSTDMCIHVCKLGODRPIKTFQGHTNEVNAIKWDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                             GNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                 .
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91.5%; Score 2488; DB 4; Length 514; 99.4%; Pred. No. 2.1e-224; rive 2; Mismatches 1; Indels
                   Best Local Similarity 99.4
Matches 469; Conservative
                  Local Similarity
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Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                                                                              Human p53 modifying protein, SEQ ID 150.
                       ABO07190 standard; protein; 514 AA
                                                                         (first entry)
                                                                         13-AUG-2003
          RESULT
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181

WO200299122-A1

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The invention relates to identifying (MI) a candidate psi pathway in polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but core the presence of the test agent bissed activity of the assay system. Drosophila) or nucleic acid with a test agent provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored), modulating (M3) a p53 pathway in amamalian cell defective in p53 function with a call with an agent that sopecifically binds an HM polypeptide or nucleic acid) and diagnosing (M3) a disease in a patient (Comprising: (a) obtaining a biological sample from the patient; (b) contacting the acontrol; and diagnosing whether the comparison indicates a likelihood disease). (M1) is useful comparison indicates a likelihood disease). (M1) is useful for diagnosing breat, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. Confidentified by (M1) are useful in a variety of diagnositic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell corrective apoptotic or cell corrective acid in the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal p53 function or progression through the cell cycle (M2) are also useful for modulating the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders in the p53 pathway such as angiogenic, apoptotic or cell proliferation disorders. The present se
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                                                                                                                                                                                                                                                                                                                                  Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGDVPSNKDVTSLDWNSEGTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to identifying (M1) a candidate p53 pathway
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ilarity 99.4%; Pred. No. 4e-224;
Conservative 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 458-459; 678pp; English.
                                                                                    2001US-0296076P.
2001US-0328605P.
2002US-0357253P.
                                         03-JUN-2002; 2002WO-US017382
                                                                                                                                                                                                                            Friedman L, Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                             pathway in Drosophila.
                                                                                                                                                                                 (EXEL-) EXELIXIS INC
                                                                                                                                                                                                                                                                          WPI; 2003-156859/15
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Matches 469; Conserv
                                                                                                                                                                                                                                                                                                N-PSDB; ACD13365
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                                                                                         05-JUN-2001;
                                                                                                               10-OCT-2001;
15-FEB-2002;
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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to breatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase continued as the protein tyrosine kinase continued a capable of pathway. Also described: (1) predicting whether a compound is capable of correlating the activity of cells, comprising obtaining a sample of cells, correlating the expression of the markers to the compound's ability to correlating the expression of the markers to the compound's ability to correlate the activity of the cells; (2) a plurality of cell lines for identifying polynucleotides and polypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polynucleotides and (cells associated with a disease state, compounds, analysing the expression pattern of a microarray of polynucleotides or polypeptides, analysing the sensitivity or resistance of cells associated with a disease state, compounds, analysing the sensitivity or resistance of cells associated with a disease state by using the correspondent of cells and polypeptides that predict the sensitivity or resistance of cells associated with a disease state by using the
                                                                                                                       360
  300
                                       300
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                                                                                                                                                                420
                                                                                                                                                                                                        420
ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                       KOOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                       ATGSYDGFARIWIKDGNLASTLGQHKGPIFALKWNKKQNFILSAGVDKTTIIWDAHTGEA
                                                                              KOOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT
                                                                                                                                                              GNILLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                                                                               GNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways.
                                                                                                                                                                                                                                                                         DSTVRLWDVDRGICIHTLITKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                                                   472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human src biomarker polypeptide SEQ ID NO:240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shaw P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 240; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                        ADD14051 standard; protein; 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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N-PSDB; ADD14646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 HESEVFICAMNPVSDLLASGSGDSTARIMNLNENSNGGSTQLVLRHCIREGGHDVPSNKD 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 VTSLDWNTNGTLLATGSYDGFARIWTEDGNLASTLGGHKGPIFALKWNRKGNYILSAGVD 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 KTTIIWDAHTGEAKQQFPFHSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTFQG 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 HTNEVNAIKWDPSGMLLASCSDDMTLKIWSMKQEVCIHDLQAHNKEIYTIKWSPTGPATS 470
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                                                                                                                                                                                                                                                                                                                                                                                                                          EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAA--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VISLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407
expression pattern of the microarray. The polynucleotides and polypeptides have cytostatic activities, and can be used in gene therapy. The polynucleotides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug sensitivity in patients to allow the development of individualized genetic profiles which aid in treating diseases and disorders (e.g. cancer) based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer: breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy, chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKD
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                                                                                                                                                                                                                                                                                                                                        1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                                                                                                                                                                                                                                 118 -----ASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 NPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVH
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                          Length 577;
                                                                                                                                                                                                                                                    82.0%; Score 2229; DB 7; Length 5'85.4%; Pred. No. 5.5e-200;
ive 32; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody preparation; cytostatic; immunomogumar
antiinflammatory; gynaecclogical; reproductive.
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                                                                                                                                                                                                              Sequence 577 AA;
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200US-0239751P.
2000US-0230583P.
2000US-0230505P.
2000US-0230514P.
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2000US-0230518P
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human MDDT SEQ ID NO 446.
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07-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABG54131-ABG56305), and also encompasses polypeptides 90% identical and polybrucleotides 93% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen conversion antigen bolymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tundurs of ovarian or breast origin; reproductive system clisorders (e.g., infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome; ovarian cysts, and dysmenorthoea), endocrine disorders, infections (e.g., chlawydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired cancer, and unimary system disorders (e.g., anaemia), cardiovascular disorders (blood-related disorders (e.g., anaemia), cardiovascular disorders (c.g., anaemia), cardiovascular disorders (c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,
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                                                                                                                                                                                                                                                                              Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. cvarian cancer), immune disorders, cardiovascular disorders and neurological diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLAS
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78.4%; Score 2132; DB 5; Length 542;
Best Local Similarity 84.8%; Pred. No. 6.5e-191;
Matches 395; Conservative 31; Mismatches 26; Indels 14
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ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 2892; 2922pp; English
                                                                                                              07-JUN-2001; 2001WO-US018569
                                                                                                                                             07-JUN-2000; 2000US-0209467P
                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI
                                                                                                                                                                                                                                             WPI; 2002-147878/19.
                                                                                                                                                                                                                                                               N-PSDB; ABQ54837
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                                             WO200200677-A1.
               Homo sapiens.
                                                                            03-JAN-2002
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                                                  215 GSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKDVTSLDWNTNGTLLATGSYD
                                                                                                                                                                                           GFARIWIXDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPF
                                                                                                                                                                                                                                                                                                 307 HSAPALDVDWQSNNTFASCSTDWCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                             CSDDWTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRL
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Flores V;

Yap PE;

Liu TF, Harris B; , Panzer SR,

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The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (1) selected from a polypeptide having a sequence selected from 254 sequences (ABP5121-ABP51464) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (1) or a biologically active or naturally occurring polypeptide comprising a sequence compound for effectiveness as an agonist or antagonist, for screening a compound for effectiveness as an agonist or antagonist, for screening a compound for preparing a polyclonal or monoclonal antibody by hybridom a technology.

**Compound for effectiveness in altering expression of a target completed comprising. Oligonucleotides and antibodies are useful for screening acompound for effectiveness in altering expression of a target compound, or a diagnostic test for a condition or a disease associated with the expression of MDDT in a biological sample, for detecting (1) in a sample, and for purifying (1) from a sample. A composition comprising (1), and agonist or antagonist is useful for treating a disease or condition or associated with aberrant expression of MDDT, where the disorders are cirrhosis, hepatitis for disease, pression of functional MDDT. (1) or (11) are useful for diagnosing, treating a disease or condition or selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, popifical such as ADDS, Addison's disease, as selected arthritis. (11) are useful for creating whockin humanised contained animals a transgenic animals to remove the remover of a ringer of a remover of animals or transgenic animals to remove the arrance of a ringer of a remover of animals of a ringer or animals a remansement of a remover of a remover of a remover of a ringer of a remover of a ringer of a remover of a ringer of a ringer of a ringer of a ringer of a remover of a remover of a ringer of a remover of a
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                                                                                                                                                                                                                                                                          Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g.
5, Lincoln SE, Altus CM, Dufour GE, Chalup MS; TL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu Thomiyama MG, Bradley DL, Rohatgi SD, Harris B; AM, Gerstin RH, Peralta CH, David MH, Panzer SI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 578; 618pp; English.
Jackson S, Lincoln SE,
Hillman JL, Jones AL,
Dahl CR, Momiyama MG,
Roseberry AM, Gerstin
                                                                                                                                                                                   WPI; 2002-527544/56
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Sequence 395 AA;

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                                                                                                                                                                                                                                                                                                                                                                                       ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA 300
                                                                                                                                                                                                                                                                                                                                                                                                                          245 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA 304
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                                                                                                     5 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
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                                                                             1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                        EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAASQ
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Length 395;
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75.3%; Score 2047; DB 5; 99.5%; Pred. No. 3.8e-183; iive 1; Mismatches 1;
                                      Matches 389; Conservative
                    Local Similarity
  Query Match
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The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). (II) especially as expressed sequence tags for identifying expressed genes therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                          305 KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 364
KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
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                                                                          361 GNLLASCSDDMTLKIWSMKQDNCVHDLQQHN
                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #21342.
                                                                                                                                                                                                               ABG21351 standard; protein; 584
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                          182 KOREATVOGEENGAHEI-NOHSKPMEIDGDVEIPPOKATVLRGHESEVFICAWNPVSDLL
                                      ASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGS
                                                                                                                                                 YDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIWDAHTGEAKQQF
                                                                                                                                                                                                            305 PFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT-------
                                                                                                                                                                                                                                                               368 KLITMTEGKRLRPKTFCSDGGALLPPAGRRPHLLTGPDIFFKRLSALFQNEVNAIKWDPS
                                                                                                                                                                                                                                                                                 GNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASF
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                                                               --AAASQQGSA
                                                                                                  KNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAMNPVSDLL
                                                                                                                                                                                                                                                                                                                    DSTVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                                                                                                                              DSTVRLWDVEQGVCTHTLMKHQEPVYSVAFSPDGKYLASGSFDKYVHIWNTQ 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ ID NO 7920
                                                              RPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAA
   Pred. No. 2.7e-152;
63.5%; Pred. .v..
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11-JUL-2000; 2000US-00614150
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  Best Local Similarity 63.5
Matches 338; Conservative
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                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ675-ABI30511), expressed DNA sequences (ABIJ6175) and the encoded proteins (ABBS7077-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGNQASTGGSNSTSTPAGGDLAAPGASQXKSQNSNEAGSSSSGNAGNANATSTDDAASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                   63.1%; Score 1715.5; DB 4; Length 700; 52.9%; Pred. No. 1.3e-151;
Disclosure; SEQ ID NO 7920; 21pp + Sequence Listing; English.
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Best Local Similarity 52.99
Matches 349; Conservative
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(first entry)

18-FEB-2002

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                              Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 18277; 1399pp + Sequence Listing; English.
           Human polypeptide SEQ ID NO 18277.
                                                                                                                                                                                                                                    Tang YT, Liu C, Drmanac RT;
                                                                                                                                                        26-FEB-2001; 2001WO-US004927
                                                                                                                                                                              28-FBB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                           WPI; 2001-514838/56.
                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                      N-PSDB; AAI84316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 208 AA;
                                                                                                            WO200164835-A2.
                                                                                       Homo sapiens.
                                                                                                                                07-SEP-2001.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, archritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences Length 208; Query Match Best Local Similarity

272 332 120 392 121 VCKLGODRPIKTFOGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKODNCVHDLQAHNK 180 9 213 HCIREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFAL KWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIH KMNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIH VCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNK HCIREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGOHKGPIFAL Gaps .. 1; Indels 41.8%; Score 1137; DB 4; 99.5%; Pred. No. 4.3e-98; ive 0; Mismatches 1; EIYTIKWSPTGPGTNNPNANLMLASAS 419 EIYTIKWSPTGPGTNNPNANLMLASAS 207 Matches 206; Conservative 273 61 333 181 g ò d δ g δ 셤

ABG21350 standard; protein; 167 AA

ABG21350

ABG21350 ID ABG2 XX AC ABG2

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGF) primers, and for chomosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites way aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patient did not appear in the printed specification, but was obtained in electronic format directly from WHOO at the printed specification, but was obtained in electronic format directly from WHOO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 PALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 RIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFFFHSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                   Human, chromosome mapping, gene mapping, gene therapy, forensic;
food supplement, medical imaging, diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMTLKIWSMKQEVCIHDLQAHNKEIYIIKWSPIGPAISNPNSNIMLA 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 51709; 103pp; English.
                                                         Novel human diagnostic protein #21341.
                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS85537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity.
                                                                                                                                                                Homo sapiens
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220 ODVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGN
                          215 SSGKTINQVICLAWSHDGNSIVIGVENGELRIWNKTGALINVLNFHRAPIVSVKWNKDGT
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                                                                                         280 FILSAGVDKTTIIWDAHTGEAKQQFPF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA13321 standard; protein; 414 AA.
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2001US-0326390P.
2001US-0328952P.
2001US-0345468P.
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2001US-0314751P.
2001US-0316752P.
2001US-0316847P.
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Lal PG, Borowsky ML,
Elliott VS, Sprague
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVA 506
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14-SEP-2001;
28-SEP-2001;
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Honchell CD,
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31-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 ISIIQKGLQYVEAEVSINEDG---TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 QAAAAAAAAAAAAAYOGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLR 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease or disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 825; 17pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.3%; Score 469; DB 6; Length 53 Best Local Similarity 25.8%; Pred. No. 1.1e-34; Matches 140; Conservative 91; Mismatches 230; Indels
                                                                                                                                                                                                                                                     Multiprotein complex; eukaryote; drug target; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kruse UD,
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1, Schultz JD, Superti-Furga GD;
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                                                                         ABR52980 standard; protein; 535 AA.
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                                                                                                                                                                                                         Protein sequence #SEQ ID 825
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                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae
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                                                                                                                   ABR52980,
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                                                    ABR52980
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335 PGPKGAIFVYQITEKTPIGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSQ 394
                                                                                    275 HIISMDVENVTILWNVISGTVMQHPELKETGGSSINAENÄSGDGSLGVDVEWVDDDKFVI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 VYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNGQVLLNLG-RSICLYTLPHHLVVIP 503
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----HSAP---ALDVDWQSNNTFAS
                                                                                                                                                                                                                                                                                                                                                                    HDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, intracellular signalling molecule, INTSIG; cell proliferative disorder; cancer, atherosclerosis; autoimmune disorder; inflammatory disorder; infection; neurological disorder; developmental disorder; endocrine disorder; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; cerebroprotective; immunosuppressive; antiinflammatory; gene therapy.
                                                                                                                                                                                  CSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCFYGHSQSIVSASWV-----GDDKVISCSMDGSVRLWSLKQNTLLALSIVDGVP
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The invention relates to 45 human intracellular signalling molecules
(INTSIG), INTSIG-1 to INTSIG-45, and the CDNAs encoding them (ADA13319-
CADA13408). The invention also encompasses expression constructs, host
cells and transgenic organisms comprising an INTSIG nucleic acid sequence
; the recombinant preparation of a INTSIG; an antibody against a INTSIG;
cethods of detection of INTSIG proteins or nucleic acids; amicro-array
containing INTSIG nucleic acids, methods of screening compounds for their
compositions comprising an INTSIG protein, an INTSIG antibody, an INTSIG
agonist or INTSIG attagonist. The INTSIG proteins, nucleic acids or
compositions comprising them are useful in diagnosing, treating or
compositions comprising them are useful in diagnosing, treating or
compositions them are useful in diagnosing, treating or
compositions the area of disorders, including call profiferative disorders
(e.g., AIDS, allergies, anaemia, asthma, bronchitis, gout, multiple
compositions comprising the arthritis, repless, strucke,
compositions dementia, or Parkinson's disease); viral, bacterial,
diagnosia, parasitic, protozoan or helminthic infections, neurological
dispressions, cancer or allowed the composition or helminthic infections in neurological
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diagnosing, treating and preventing diseases or conditions associated with the aberrant INTSIG expression e.g. cancer, diabetes, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represents an INTSIG protein of the invention.
                                                                                                                       Claim 1; Page 225-226; 367pp; English.
                                                              infections.
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Seguence 414 AA

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                                                                                                                                                                                                                                                                                    260 CAEISSASFNW-----DCSLILTGSMDKTCKLWDATNGKCVATLTGHDDEILDSCFDY 312
                                                                                             ---TLEGHRNVVYAIAFNNPYGDKIATG
                                                                                                                             SGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDG
                                                                                                                                                 1.54 SFDKTCKLWSVETGK-----CYHTRR-----GHTAEIVCLSFNPQSTLVATGSMDT
                                                                                                                                                                                                                                                                                                                                        248 FARIWIKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH
                                                                                                                                                                                                                     200 TAKLWDIONGEELTLRGHSAEIISLSFNTSGDRIITGSFDHTVVVWDADTGRKVNILIGH
                                                                                                                                                                                                                                                      SA--PALDVDWQSNNTFASCS---IDMCIHVCKL---GQDRPIKTFQGHTNEVNAIKWDP
                                                               129 NTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAW-NPVSDLLASG
                                                                                                                                                                                                                                                                                                                   TGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASAS
                                   Gaps
                                 92
   Length 414;
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   ,DB 6;
13.8%; Score 374.5; DB 6; 28.3%; Pred. No. 5.7e-26; iive 49; Mismatches 137;
                               Conservative
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Query Match
Best Local Similarity
Matches 99; Conserv
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ABB62260 standard; protein; 411 26-MAR-2002 ABB62260, RESULT 12 ABB62260 ID ABB6 XX AC ABB6 XX XX DT 26-M XX XX

Drosophila melanogaster polypeptide SEQ ID NO 13572.

SAKNGENTANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVLRGHESEVFICAMNPVSD 182 TGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIK 356 PNAN---LMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKC 465 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences LMVSASEDATIRIWDFETGEYERSLKGHTDSV-----QDVA-----FDAQGK LLASCSADLSIKLWDFQQSYECIKTMHGHDHNVSSVAFVPAGDYVLSASRDRTIKMWEVA VHIEGSIFATCSNDQTIRVWLTNSKDCKVELRDHEHTVECIAWAPEAAASAINEAAGADN **EELNQAIADYLGSNGYADSLETFRKEADLSTEVEKKFGGLLEKKWTSVIRLQKKVMELEA** EVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAASQQG LLASGSGDSTARIWNLS----ENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGT LLATGSYDGFARIW--TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAH 357 WDPTGNILLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP------TGPGTNN DEVNFLVYRYLQESGFSHSAFTFGIKSHIS---QSNINGALVPPAALISIIQKGLQYVEA Drosophila, developmental biology; cell signalling; insecticide; pharmaceutical. Indels 163; Disclosure; SEQ ID NO 13572; 21pp + Sequence Listing; English Length 411; -----KEVIE------13.6%; Score 370.5; DB 4; 22.4%; Pred. No. 1.3e-25; iive 77; Mismatches 158; EN; PWD, 23-MAR-2001; 2001WO-US009231. 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. ::: | KLTEAE-------검 Conservative Drosophila melanogaster. TG------Adams M, 2001-656860/75 Similarity (PEKE) PE CORP NY WPI; 2001-656860 N-PSDB; ABL06363 Sequence 411 AA; WO200171042-A2 interactions. 115; 27-SEP-2001 Venter JC, ø 63 123 122 297 Query Match Best Local S 183 164 Best Loca Matches %XCCCCCCCCCXXXXIXXBXXBXXBXXBXXBXXBXX8XX g 8.8 ò à 9 ò 유 à ð

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303 KKGHQGPFLASGSRDKTIRIMDVSVGLCLLTLSGHDNWVRGLAFHPGGKYLVSASDDKT 362
                                                                                                                                                                                                                                                                                                      TZap; T cell activation; immune response; transplant rejection;
bone marrow transplantation; rheumatoid arthritis; lupus erythematosis;
buntiple sclerosis; encephalitis; vasculitis; diabetes mellitus;
pancreatitis; gastritis; thyroiditis; malignant disorder; asthma;
lepramatosis; gastritis; skin tumour; adrenal tumour; lung tumour;
wound healing; growth disorder; inflammatory disease; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide encoding TZap protein involved in T cell activation, useful for diagnosing and treating diseases involving T cell activation, for treating organ transplantation rejection, rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                    rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "unspecified residue encoded by NTC
                                                                                                                                                                                                                                                                        of a human TZap gene cDNA clone.
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                                                                                      ----DLRNKRCMKTLYAH 380
                                                   466 VHIWNTQVCLHYLNGQVLLNLGRSICLYTLPHH
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inflammatory and/or infectious diseases
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                                                                                                                                                                        AAB68284 standard; protein; 485
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25-FEB-2000; 2000US-0185016P.
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                                                                                                                                                                                                                                          (first entry)
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N-PSDB; AAF85075.
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AAB68284
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Gaps

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Indels

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Human; guanosine triphosphate binding associated protein; GTP; GBAP; inflammation; AIDS; Addison's disease; anaemia; arteriosclerosis; asthma; autoimmune disorder; hepatitis; multiple sclerosis; cancer; diabetes; osteoporosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel human guanosine triphosphate (GTP) -binding associated proteins (GBAPs; AAB68501-AAB68566) and their coding sequences (AAF58301-AAF58366). The proteins and coding sequences of the
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asthma.
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                                                                          165 LRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSEN----STSGSTQLVLRHCIREGGQ
                                                                                                                 IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFH--
                                                                                                                                              230 INDTTAGRCERILIGHTQSVTCLRWGGDG-LLYSASQDRTIKVWRAHDGVLCRTLQGHGH
                                                                                                                                                                             -----QSNNTFASCS
                                                                                                                                                                                                      289 WVNTMALSTDYALRTGAFEPAEASVNPQDLQGSLQELKERALSRYNLVRGQGPERLVSGS
                                                                                                                                                                                                                                   327 TDMCIHVCKLGQD-RPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVH
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                                                        ----NKDVTSLDW-----NSEGTLLATGSYDGFAR
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Patterson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JL, Lal P,
, Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GTP-binding associated protein #16.
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Lu DAM,
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99US-0150460P.
99US-0159849P.
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Baughn MR,
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                                                                                                                                                                             --SAPALDVDW-----
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N-PSDB; AAF58316.
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23-AUG-1999;
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                                                                                                                                                                                                               349 DDFTLFLWSPAEDKKPLTRMTGHQALINQVLFSPDSRIVASASFDKSIKLWDGRTGKYLA
                                                                                                                                                                      LEGHSEAVISVAFSPIGKYLASGSGDTTVRFWDLSTETPHFTCKGHRHWVLSISWSPDGK
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present invention are useful for treating a variety of disorders including inflammation, AIDS, Addison's disease, anaemia, arteriosclerosi, antenina, autoimmune disorders, Grave's disease, hepatitis, multiple scherosis, cancer, diabetes, osteoporosis and
                                                                                                                       : 68
                                                                                               Length 485;
                                                                                                                      47; Mismatches 145; Indels
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, Otsuki
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                                                                                               Score 366.5; DB 4
Pred. No. 4.2e-25;
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Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:11400
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26.8%;
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11-JAN-2000; 2000JP-00118776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                       103; Conservative
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                                                                                              Query Match
Best Local Similarity
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                                                                        Sequence 485 AA;
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Ishii S,
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The present invention describes primer sets for synthesising 5602 full-
length CDMAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonuclectide comprises as least 15 nucleotides; or. (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence of an another comprises a 1'-end sequence of 2'-end sequence 3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDMAs. The primers are also useful for the particularly full-length cDMAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the full-length cDMAs. The primers are also useful for the contains encoded by the full-length cDMAs. The primers are also useful for the contains and another and sequences, and AAH13622 to AAH13622 represent human amino acid sequences; and AAH13622 to AAH13622 represent contains and the exemplification of the contains and the exemplification of the contains and the exemplification of the contains and the exemplification of the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and the contains and contains and contains and contains and contains and contains and contains and co
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                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                                                                                ID NO 11400; 2537pp + Sequence Listing; English.
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DLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPV

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289 WVNTMALSTDYALRTGAFEPAEASVNPQDLQGSLQELKERALSRYNLVRGQGPERLVSGS

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AAGS 2000 A AGS 2000 A	ALIC	Nos isio isio C.P to, e of 2159		> 1	VLRHCIR	IFALKWN : ::: VNSVVFN	-ASCSTD 	NCVHDLQ : ECLYTFL	QEPVYSV
0000000000000000		d] - 0 7120 7120 olk, gimot UlD:2	% % . % 	VDGD RLWD	STOL HISW	HKGP HTSW	GSM	MKQD : ISSG	E
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64 66 6 66 66 66 66 66 66 66 66 66 66 66		RESULT 1 AC2239 WD-40 repeat protein C;Species: Nostco sp. A;Note: Nostco sp. C;Accession: AC2239 C;Accession: AC2239 Nakazaki, N.; Shimpo DNA Fes. B; 205-213, A;Title: Complete Gen A;Reference number: A;Accession: AC2239 A;Accession: AC2239 A;Accession: AC2230 A;Accession: AC2230 A;Accession: AC2230 A;Accession: AC2230 A;Accession: AC2230 A;Accession: AC2230 A;Accession: AC2230 A;Accession: AC2230 A;Corserimental source C;Genetics: Afgenetics: CA	Query Match Best Local Si Matches 119;	136 N 1127 N	195 I) : 1184 L	251 II : 1226 LI	310 P	363 Li	423 T
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WD-repeat protein

S48052 AB2202 S36113 AE1861 AG2375 S19487

T02617 S05357 T00798

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                                                                                 Disobble membrane protein YBR103w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein YBR0832
C;Species: Saccharomyces cerevisian Drotein YBR0832
C;Species: Saccharomyces cerevisian 01-Sep-1995 #text_change 19-Apr-2002
C;Date: 01-Aug-1995 #sequence revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: $48268; $45971; $44683
R;Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vetter, I.; Feldmann, H.
A;Atile: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Atile: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A;Atcession: $48268
A;Atcession: $48268
A;Status; nucleic acid sequence not shown
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A;Residues: 1-535 <MAN>
A;Residues: 1-535 <MAN>
A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55606.1; PID:g476059
R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSITSEELNYLIWRYCQEMGHEVSALALQDETRVLEFDEKYKEHI-------PLGTL
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17.4%; Score 472; DB 2; Length 53
Best Local Similarity 25.8%; Pred. No. 2.8e-26;
Matches 140; Conservative 91; Mismatches 230; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-535 <FE2>
A;Cross-references: EMBL:235972; MIPS:YBR103w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSISSDEVNFLVYRYLQESGFSHSA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: SGD:S0000307
                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: S45927; Accession: S45971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Map position: 2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: SGD:SIF2
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AF2071

WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001

C;Date: 14-Dec-2001

R;Raneko, T: Nakamura, Y:, Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2071

A;Status: preliminary

A;Residues: 1-1683 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Kazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8 205-213, 2001

DNA Res. 8 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anat A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                         WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
(Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: A12155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 LRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1258 «KUR»
A;Crossreferences: GB:BA000019; PIDN:BAB74499.1; PID:g17131893; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1100 -----LRGHSNRVYSAIFSPNGEIIATGSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNFILSAGVDKTTIIWDAHTGEAKOOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ccigrcvgi----
445 IFAGRISQDGQKYAVAFMDGQVNVYD----LKKLNSKSRSLYGNRDGILNPLP----IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 QDRPIKTFQCHTWEVNAIKWDPTGNLLASCSDDWTLKIWSMKQDNCVHDLQQHNKEIYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       974 LEGHTDFIYGIAFSPDSQTLASASTDSSVRLWNI---STGQCFQILLEH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.9%; Score 458.5; DB 2; 32.0%; Pred. No. 8.5e-25; iive 43; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1204 ASGSQDQTVRIWNVKTGECLQILRAKRL 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 ASGSFDKCVHIWN--TOVCLHYLNGOVL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1074 GOLLASASADOSVRLWD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                           496 LYA 498
                                                                              504 LVA
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DD 834 CGEDRSIKLWDIQRGECVNTLWGHSSQVWAIAFSPDGRTLISCSDDQTARLWDV 887 QY 156 EIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCI 215 B88 -ITGNSLNILRGYTRDVYSVAFSPDSQILASGRDDYTIGLWNLKTGECHPL 937 QY 216 REGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGGHKGPIFA 271	Db 992 UVESPDGHTLASSSEDRTIRLWDKDTGDCLQCLKGHSHWVWTVAFSPDGRILASGSADSE 1051 Qy 331 IHVCKLGQDRPIKTFQGHTNEVNALKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQH 390 1052 IKIWDVASGKCLQTLTDPQGMIWSVAFSLDGTLLASASSEDQTVKLWNLKTGECVHTLKGH 1111 Qy 391 NKEIYTIKWSPTGPGTNNPNANLALASASFDSTVRLWDVDRGICHTLTK-HQEPVYSVA 449 1112 EKQVYSVAFSPNGQIAASGSEDTTVKLWDISTGSCVDTLKHGHTAAIRSVA 1162 Qy 450 FSPDGRYLASGSFDKCVHIWNVC 474 Db 1163 FSPDGRLLASGSEDEKIQLWDWQNC 1187	RESULT 6 A1493 WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species Nostoc sp. PCC 7120 C;Species Nostoc sp. PCC 7120 C;Species Nostoc sp. Strain PCC 7120 C;Species Nostoc sp. Strain PCC 7120 C;Species Nostoc sp. Strain PCC 7120 C;Accesion: A1493 C;Accesion: A1493 C;Accesion: A12493 C;Accesion: A1493 A;Accesion: A1	170 #	-E -E -E -E -E -E -E -E -E -E -E -E -E -
Cross-references: GB:BA000019; PIDN:BAB73823.1; PID:g17131215; GSPDB:GN00 Experimental source: strain PCC 7120 Genetics: Jenetics: Jenet	Db 1245 LSFSPDGRTLASASADKTIKLWRIADGKLVKT-LKGHNDSVWDVNFSSDGRAIASASRDN 1303 Qy 123 SAKNGENTANGEENGAHTIANNHTDWMEVDGDVEIPPNKAVVLRGHESEVFICAWNFVSD 182 1304 TIK	Db 1440 KTLIGHDNEVNKYPEDGKTLASASRDNITKIMNYSDGKFKKTLKGHTDEVFWYSFEPD 1499 Qy 361 GNLLASCSDDMTLKIWSKODCKTLAOQHNKEITKWSPTGFGTNNPNANLMLASASF 420 Db 1500 GKIIASASADKTIRLWDSFSGNLIKSLPAHNDLVYSVNFNPDGSMASTSA 1550 Qy 421 DSTVRLWDVDRGICHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNG 480	C;Accession: AE1810 Nakazaki, N.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA, Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AE1810 A;Accession: AE1810 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1227 KUR> A;Cross-references: GB:BA000019; PIDN:BAB77553.1; PID:g17135007; GSPDB:GN00179 A;Experimental source: strain FCC 7120 C;Genetics: A;Gene: alr0029	Query Match Best Local Similarity 29.2%; Pred. No. 8.4e-24; Best Local Similarity 29.2%; Pred. No. 8.4e-24; Matches 130; Conservative 73; Mismatches 171; Indels 71; Gaps 15; Qy 64 VSINEDG-TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAA 117 Db 780 VSFSPDGQTLASSGEDSTVRLWDVKTGQCWQIFEGHSKKVYSVFFSPDGQTLAS 833 Qy 118 ASQQCSAKNGENTANGEBNCAHTIANNHTDMMEVDGDV 155

12;

Gaps

Indels

Length 1356;

870

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1010 GSVWSVAFSPDGQRVASGSDDKTİKIWDTASGTCTQİLEGHGGWVQSVVFSPDGQRVASG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 STARIWNLSENSTSGS-TQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 SDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              905 KTIKIW----DAASGTCTQTLEGH----GGR-----VQSVAFSPDGQRVASGSDDHTI
A;Cross-references: EMBL:L28125; NID:g607002; PID:g607003; PIDN:AAA85775.1
C;Genetics:
A;Gene: het-el
A;Introns: 761/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             820 ISTISVVEAEWNACTOT-----LEGHGSSVLSVAFSADGQRVASGSDDKTIKIWDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDDHTIKIWDAVSGTCTQTLEGHGDSVWSVAFSPDGQ------RVASGSIDGTIKIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAASGTCTQTLEGHGGWVHSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEG 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAASQQGSAKNGE-----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWN--TQVCLHYLNG 480
                                                                                                                                                                                                                                                                                                                                                     15.5%; Score 420.5; DB 2;
llarity 28.2%; Pred. No. 5.2e-22;
Conservative 63; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      871 ASG--TGTOT-----
                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
117; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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T18521
beta transducin-like protein - Podospora anserina
C;Species: Podospora anserina
C;Species: Podospora anserina
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18521
R;Saupe, S:; Turcq, B:; Begueret, J.
R;Saupe, S:; Turcq, B:; Begueret, J.
A;Title: A gene responsible for vegetative incompatibility in the fungus Podospora anser
A;Reference number: Z18944; MUID:96009891; PMID:7557402
A;Accession: T18521
A;Accession: T18521
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1356 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp. PCC 7120
A.Nostoc sp. strain PCC 7120
C.Species: Nostoc sp. strain PCC 7120
C.Species: Nostoc sp. strain PCC 7120
C.Species: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C.Spacession: Als B66
C.Spacession: Als B66
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A Modecule type: DA
A Modecule type: DA
A Residues: 1-1708 «KUR»
A; Cross-references: GB:BA000019; PIDN:BAB72436.1; PID:g17129823; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Gen
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15.7%; Score 426; DB 2; Length 17
Best Local Similarity 32.1%; Pred. No. 2.9e-22;
Matches 110; Conservative 61; Mismatches 130; Indels
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                                        DGRYLASGSFDKCVHIWN--TQVCL
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1062 IGKGVCVRTFSGH 1074
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. B, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD1842
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A,Residues: 1-1711 <KUR>
A,Cross-references: GB:BA00019, PIDN:BAB77808.1; PID:g17135262; GSPDB:GN00179
A,Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1711;
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15.0%; Score 40%; DB 2; L.
Best Local Similarity 26.2%; Pred. No. 5.7e-21;
Matches 125; Conservative 76; Mismatches 182;
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AC1842
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Specesion: AC1842
C,Accession: AC1842
Nakazaki, N.; Shimpto, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA, Res. B, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A,Reference number: AB1807; MUID:21595285; PMID:11759840
A,Status: preliminary
A,Accession: AC1842
A,Status: preliminary
A,Cross-references: GB:BAOC0019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179
A,Genetics:
A,Genetics:
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A,Genetics:
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                                                                                                -LASASFDSTVRLWDV -- DRGICI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 NFILISAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLG 337
592 GNDKTAKIWKLNSPNSIIVRGHEDEVPDLVFSPNGKYIATASWDKTAKLWSIVGDKLQEL 651
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N;Alternate names: protein sl10163
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;bate: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 395; DB 2; Length 174
28.2%; Pred. No. 5.1e-20;
ive 59; Mismatches 131; Indels
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                                                                                                                                                                                                                     HILTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWN 470
                                                                                                                                                                                                                                                  165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNL-
                                                                                             -------INNPNANLM------
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G.Species: Nostoc sp. PCC 7120

A.Note: Nostoc sp. strain PCC 7120

G.Species: Sp. strain PCC 7120

G.Species: Sp. strain PCC 7120

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G.Species: Sp. strain PCC 7120

G.Species: Sp. strain PCC 7120

G.Species: Sp. strain PCC 
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                                                                                                                                                                                                                                                                                                                                                                   1519 VTDIKFSADGKNIVSASADKTIKIWSL-DGRLIRTLOGHSASVWSVNLSPDGOTLASTSO 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                            369
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A, Residues: 1-934 < KUR>
A, Cross-references: GB:BA000019; PIDN:BA372622.1; PID:g17130010; GSPDB:GN00179
A, EXPERIMENTAL SOURCE: strain PCC 7120
C, Genetics:
A, Gene: all0664
                                                                                                                                                                                 IWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                DMTLKIWSMKQDNCVHDLQQHNXEIYTIKWSPIGPGINNPNANLMLASASFDSTVRLWDV 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHTGEAKQOFPFHSAPALDVDWQ----SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1628 PNGTILKTFQGHRGGVRSVSFSPDGKILASGGHDTTVKVWNLEGIELQTLNLDELLN 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRGICHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ-VCLHYLNGQVLLN 485
                                                                                                          .403 NDGKKITSLSTDSTWKTWSLDGKLLQTLSSPLP---DVTSISFTPDNKIVALASPDHTIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLSENSTSGSTQLVLRHCIREG-----GQDVPSNKDVTSLDWNSEGTLLATGSYDGFAR
                                                                                                                                                                                                                                                                                                            311 ALDVDWQSN-NTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AISSSAESFINANLEF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 SKFIATASRDKTVK-----IWSLDGKKQL----VVLREEKGEGFNSVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQ--DVPSNKD-VTSLDWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.9%; Score 404.5; DB 2; Length 934;
Best Local Similarity 24.1%; Pred. No. 4.4e-21;
Matches 124; Conservative 104; Mismatches 176; Indels 111;
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377 SPDGTLMATGSWDNTAKIWS--
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                                                                                                                                                                                                                                                                                                     A,Accession: S76086
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Festidues: 1-1693 «KMA)
A,Cross-references: EMBL:D63999, GB:AB001339; NID:g1001396; PIDN:BAA10064.1; PID:d101071
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C,Superfamily: unassigned WD repeat bomology «WDOL»
F;1091-1084/Domain: WD repeat homology «WDOL»
F;1092-1125/Domain: WD repeat homology «WDOL»
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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T40883
Who repeat protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40883
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
Submitted to the BMBL Data Library, September 1998
A;Reference number: Z21954
A;Reference number: Z21954
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                                                                                                                                                                                                                                                           Reference number: 874322; MUID:97061201; PMID:8905231
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14.5%; Score 394.5; DB 2;
Best Local.Similarity 28.2%; Pred. No. 5.3e-20;
Matches 115; Conservative 55; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology <WD07>
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F;1625-1658/Domain: WD
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F;1174-1207/Domain:
F;1256-1289/Domain:
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F;1338-1371/Domain:
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E;1502-1535/Domain:
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-564 <WOO>

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AB2410

Who respeat protein [imported] - Nostoc sp. (strain PCC 7120)

C,Species: Nostoc sp. PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120

C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C,Accession: AB2410

R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A, Reference number: AB1807; MUID:21595285; PMID:11759840
A;Cross-references: BMBL:AL031764; PIDN:CAA21113.1; GSPDB:GN00068; SPDB:SPCC1235.09
A;Experimental source: strain 972h-; cosmid c1235
C;Genetics:
A;Gene: SPDB:SPCC1235.09
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1551 «KUR»
A,Cross-references: GB:BA000019, PIDN:BAB76533.1, PID:g17133971, GSPDB:GN00179
A,Experimental source: strain PCC 7120
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14.0%; Score 381; DB 2; Length 1551;
Best Local Similarity 23.4%; Pred. No. 4.4e-19;
Matches 118; Conservative 94; Mismatches 175; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                    564;
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Best Local Similarity 24.4%; Pred. No. 8.5e-20;
Matches 131; Conservative 106; Mismatches 198;
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C,Genetics:
A,Gene: all4834
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OY 168 HESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGSTOLVLRHCIREGGODVPSNKD 227 Db 390 HASDVNSYSPROEFICAGSDDKIIKWNLKKNKOKIHTLEGHGG 434 OY 228 -UTSLDWNKSGTLLATGSDDKIIKWNLKKNTLGQHKGPIFALKWNKKGNFI 281 Db 435 WVWALTASTGADLATTKNNLATGKEIRHLKGBSGOVASVAFSPDGKTL 490 OY 282 LSACUDKTITIMDAHTGBAKQOFPHSAPALDVDWO-SNNTFASCSTDMCHIVCKLGDPR 340 1	
0y 48 ALISHIQKGLQYVEAEVSINEDGTLFPGREISLIDAVMPDVOTROQAYRDKLAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	RESULT 15 AH3195 AH3195 AH3195 AH3195 AH3195 C. Sabadots Nostoc sp. PCC 7120 C. Species: Nostoc sp. PCC 7120 C. Species: Nostoc sp. PCC 7120 C. Species: Nostoc sp. PCC 7120 C. Species: Nostoc sp. Strain PCC 7120 C. Sacanoto. Sp. Strain PCC 7120 C. Sacanoto. Sp. Strain PCC 7120 C. Sacanoto. Sp. Strain PCC 7120 C. Sacanoto. Sp. Strain PCC 7120 C. Sacanoto. Sp. Species C. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sacanoto. Sp. Sp. Sp. Sp. Sp. Sp. Sp. Sp. Sp. Sp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August Run on:

9, 2004, 16:40:42; Search time 8.66667 Seconds (without alignments) 3088.161 Million cell updates/sec

Title: Perfect score:

US-09-987-701-4 2718 1 MSISSDEVNFLVYRYLQESG......LPHHLVVIPLVALIELLVLK 514 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	1 4	91.7	514	-	TBLR HUMAN	O9bzk7 homo sapien
7	2229	82.0	526	Н	1	homo
m	17	σ.	522	н	TBLY HUMAN	homo
4	1308	48.1	313	Н	TBLX MOUSE	mus ก
ß	7	7.	1526	٦	YY46_ANASP	Q8yril anabaena sp
φ	47	۲.	535	Н	1 1	saccharom
7	58.	9	1258	Н	YSOO ANASP	Q8ytc2 anabaena sp
89	51.	œ	1683	Н	1 1	anabaena
	20.	'n.	1356	Н		podospora
	94.	4.	1693	Н	Y163_SYNY3	
	99	m m	485	Н	HUS7_HUMAN	Q9nvx2 homo sapien
	65.	'n.	485	Н	HUS7_MOUSE	mus n
13	351.5	N.	409	Н		P43034 homo sapien
	50.	'n	409	Н		bos t
	IU.	ά.	339	Н	CIA1_HUMAN	076071 homo sapien
		'n	409	Н	LIS1 MOUSE	mus m
	m	'n	800	H	T2D4_HUMAN	Q15542 homo sapien
	m	ς,	515	Н	YCW2_YEAST	sacch
	m	ά.	742	Н	PKWA_THECU	
	•	ά.	361	Н	WDS DROME	
	33	'n	437	Н	AAC3_DICDI	_
		ď.	334	Н	WDR5_HUMAN	
	19.	Ή.	909	Н	PF20_CHLRE	-
	-1	Η.	579	Н	SE10_CAEEL	_
	31	Ξ.	605	Н	POF1_SCHPO	P87053 schizosacch
		ή.	376	Н	YKY4_CAEEL	_
	0	٠	704	Н	T2D4 DROME	P49846 drosophila
	0		798	Н	T2D4_YEAST	Ø
	0	٠	665	П	LI23_CAEEL	Q09990 caenorhabdi
	0	٠	501	Н	YH92_CAEEL	Q23256 caenorhabdi
	299	11.0	640	Н		
	29	10.7	1191	Н	Y143_SYNY3	
		•	395	Н	· •	

Q9uug8 schizosacch	P54314 mus musculu OOO659 emericella	Q9y297 homo sapien	Q93847 caenorhabdi	Q9ukb1 homo sapien	Q9fuy2 arabidopsis	P56094 kluyveromyc	022212 arabidopsis	P49178 zea mays (m	Q09715 schizosacch	043172 homo sapien
TU12_SCHPO	SCOB FRENT	FW1A_HUMAN	YZLL CAEEL	FW1B HUMAN	LUG ARATH	TUP1 KLULA	PRP4 ARATH	GBB MAIZE	TU11 SCHPO	PRP4_HUMAN
Н.	-1	1 ~	Н	Н	~1	Н	Н	H	Н	Н
586	η ν Ο α	605	395	542	931	682	554	380	614	522
10.6	10.6	10.5	10.4	10.4	10.4	10.4	10.3	10.3	10.3	10.3
288.5	286	285	283	283	283	282.5	281	280.5	280	279
34	3 6	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licensee.ed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND INTERACTION WITH HDAC3.
MEDLINE=21930350; PubMed=11931768;
Zhang J., Kalkum M., Chait B.T., Roeder R.G.;
"The N-COR-HDAG3 nuclear receptor corepressor complex inhibits the JNK pathway through the integral subunit GPS2.";
Mol. Cell 9:611-623(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
Submitta Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMDINIT: Interactes with HDAG-C3.
-!- SIMDINIT: Lish domain.
-!- SIMILARITY: Contains 8 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang X., Dormady S., Basch R.;
"Identification of four human to by early hematopoietic progenitors.";
Submitted (MAY-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            Q9BZX7; Q9H2I1; Q9H9A1;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Nuclear receptor co-repressor/HDAC3 complex subunit TBLR1 (TBL1-related protein 1).
                                                                              514 AA.
                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF214544; AAK00301.1; --
EMBL; AF268193; AAG44736.1; --
EMBL; AK02296; BAB14331.1; --
InterPro; IPR006594; LisH.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
PRINTS; PR00320; GPROTEINBRPT.
Prodom; PD000018; WD40; 3.
SMART; SM00667; LisH; 1.
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                        (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         TBLR1 OR IRA1.
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                              TBLR HUMAN
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transducin beta-like 1x protein (Transducin-beta-like 1, X-linked)
FBLIX OR TBLI.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-> H (IN REF. 3).
-> Q (IN REF. 2).
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Pred. No. 2.4e-174;
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                 PROSITE; PS50896; LISH; 1.
PROSITE; PS0678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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   SM00320; WD40; 8.
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Best Local Simil
Matches 470; C
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SEQUENCE FROM N.A.

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                                                                                                                                                                                       MEDLINE=99264241; PubMed=10330347; Bassi M.T., Ramesar R.S., Caciotti B., Winship I.M., De Grandi A. Riboni M., Townes P.L., Beighton P., Ballabio A., Borsani G.; "X-linked late-onset sensorineural deafness caused by a deletion involving OA1 and a novel gene containing WD-40 repeats."; Am. J. Hum. Genet. 64:1604-1616(1999)
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GO: GO:0007165; P:signal transduction; TAS.
GO: GO:0007601; P:vision; TAS.
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PROSITE; PS50678; WD REPEARS_1; 4.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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EMBL; BC032708; AAH32708.1; -..
Genew; HGNC:11585; TBL1X.
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MEDLINE=22388257; PubMed=12477932;
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ProDom: PD000018; WD40; 3.
SMART; SM0067; LisH; 1.
SWART; SM00320; WD40; 7.
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InterPro; IPR001680; WD40.
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                                                                                                                                                                                     BAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAA--- 117
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last semocation update)
Transducin beta-like 1Y protein (Transducin-beta-like 1, Y-linked)
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"The DNA sequence of the human Y chromosome.";
Submitted (DEC-2000) to the EMBL/Genbank/DDBJ databases.
-! SIMILARITY: Contains 1 LisH domain.
-! SIMILARITY: Contains 8 WD repeats.
                                                   14;
       Length 526;
                                                 Indels
Query Match
82.0%; Score 2229; DB 1;
Best Local Similarity 85.4%; Pred. No. 4.4e-155;
Matches 414; Conservative 32; Mismatches 25;
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61 BAEISINKDGTVFDSRPIESLSLIVAVIPDVVQMRQQAFGEKLTQQQASAAATEASAMAK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AATMTPAAISQQNPPKNREATVNGEENGAHEI-NNHSKPMEIDGDVEIPPNKATVLRGHE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEVFICAWNPVSDILASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVPSNKDVT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSITSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGTLVPPSALISILQKGLQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 ----AAASQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 SLDWNSDGTLLAMGSYDGFARIWTENGNLASTLGQHKGPIFALKWNKKGNYVLSAGVDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIIWDAHTGEAKQQFPHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 TIIWDAHTGEAKQQPFFHSAPALDVDWQNNMTFASCSTDMCIHVCRLGCDHPVKTFQGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 BAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 SEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 NANLMLASASFDSTVRLWDVDRGICIHTLITKHQEPVYSVAFSPDGRYLASGSFDKCVHIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2170; DB 1; Length 52
Pred. No. 8.7e-151;
?: Mismatches 33; Indels
                                                                                                                                                                                                                                LISH.
WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 5.
WD 6.
WD 7.
WD 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Mismatches
                                                                                                                                                                                                     ij
                                                                                                                                              PROSITE; PS50896; LISH; 1.
PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                           Pfam; PF00400; WD40; 8.
PRINTS; PR00320; GFROTEINBRPT.
ProDom, PD000018; WD40; 3.
SWART; SM0067; Liest; 1.
SWART; SM00320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                         56688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           79.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                           84.1%;
EMBL; AF332222; AAK13474.1;
              Genew, HGNC:18502, TBL1Y.
InterPro, IPR006594; LisH.
InterPro, IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           406; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                      36
216
272
313
313
354
447
521
                                                                                                                                                                                                                                                    2333
2333
2314
3316
3357
4450
7491
7491
                                                                                                                                                                                                                    Repeat; WD repeat.
DOMAIN 4
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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16-OCT-2001
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TBLX MOUSE Q9QXE7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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TBLX MOUSE
ID TBLX M
AC Q9QXET
DT 16-0CT
DT 16-0CT
DT 10-0CT
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SEQUENCE FROM N.A.
MEDLINES-2159-2985, PubMed=11759840,
MEDLINES-2159-2985, PubMed=11759840,
Kanacko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Natsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
                                                                   Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
(Rel. 41, Last annotation update)
               Hypothetical WD-repeat protein alr3466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WD 3. WD 3. WD 4. WD 5. WD 5. WD 5. WD 6. WD 7. WD 9. WD 9. WD 11. WD 112. WD 12. WD 12. WD 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AP003593, BAB75165.1; -.
BIR; ACC2959, ACC239.
INCEPPC; IPR007111; NACHT_NTPASE.
INCEPPC; IPR001680; WD40.
                                                   7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                   (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . protein; R
334 376
823 862
862 901
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1069
1111
11153
11237
1237
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1450 149
1526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 119; Conserv
                                                                                NCBI_TaxID=103690;
                                                       Anabaena sp.
28-FEB-2003
                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 GSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEYG-----QKSNLASTLGQHKGPIFALKWNKKGNYILSAGVDKTTIIWDAHTGEAKQ 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 NILASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGDSTARININENSNGGSTQLVLRHCIREGGHDVPSNKDVTSLDWMWEHCWQQVPMWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFPFHS-APALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQV 473
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                               Botcherby M.R.M., Straw R., Clarke D., Greystrong J.S., Weston Hunter G., Kimberly C., Kindse M., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ:databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%; Score 1308; DB 1; Length 313; 83.2%; Pred. No. 3.2e-88; ive 16; Mismatches 19; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34808 MW; 3BC48683432DFEF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1526 AA
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(Rel. 41; Last sequence update)
   Transducin beta-like 1X protein (Fragment).
TBL1X OR TBL1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0320; GPROTEINBRPT.
ProDom; PD000018; WD40; 2.
SMART; SM00320; WD40; 5.
PROSITE; PS00678; WD REPEATS 1; 3.
PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50244; WD REPEATS 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M M M M 1.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; F38006; CAB61534.1; -. MGD; MGI:1336172; Tblix. InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 5.
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115
198
249
291
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313
313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat, WD repeat.
NON TER
REPEAT <1
REPEAT 160
REPEAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=10090;
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ID YY46 ANASP
AC Q8YRII;
DT 28-FBB-2003 (
DT 28-FBB-2003 (
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nes 243;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1127 NGV-TLANGSSDQIVRLWD--ISSKKCLYTLQGHTNWVNAVAFSPDGATLASGSGDQIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 NGAHTIANNHTDMMEVDGDVEIPPNKAV-VLRGHESEVFICAWNPVSDLLASGSGDSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 IWNLSENS----TSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
"Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-i- SIMILARITY: Contains 16 WD repeats.
-i- SIMILARITY: Contains 1 pentapeptide repeat domain.
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PRINTS; PR00320; GPROTEINBRPT.
PRINTS; SW00320; WD40; 8.
SWART; SW00320; WD40; 8.
PROSITE; PS00678; WD4 REPEATS 1; 11.
PROSITE; PS50024; WD REPEATS 2; 15.
PROSITE; PS50294; WD REPEATS REGION; 1.
PROSITE; PS50394; WD REPEATS REGION; 1.
Hypothetical protein; Repeat; WD repeat; Complete proteome.
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PENTAPEPTIDE
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EMBL, X78993; CAA55606.1; EMBL, Z35972; CAA85058.1; PIR, S48268; S48268. GermOnline; 138646; -. SGD; S0000307; SIF2.

R GO; GO: 0005634; C: nucleus; IPI.
R GO; GO: 0005634; C: nucleus; IPI.
R GO; GO: 0005634; C: nucleus; IPI.
R GO; GO: 0017136; F: NAD-independent histone deacetylase activity; IDA.
R GO; GO: 0015675; F: NAD-independent histone deacetylase activity; IDA.
R GO; GO: 0016575; P: nistone deacetylation; IDA.
R GO; GO: 0016575; P: histone deacetylation; IDA.
R GO; GO: 0016575; P: nistone deacetylation of transcription from P. . .; IPI.
R GO; GO: 0000122; P: negative regulation of transcription from P. . .; IPI.
R InterPro; IPR004680; W440.
R InterPro; IPR004080; W440.
R ProDom; PD000018; W400; I.
R SMART; SM00567; Lish; I.
R SMART; SM00220; W440; I.

repeat; Chromatin regulator; Nuclear protein

PS50896; LISH; 1. 8900678; MD_REPEATS 1; FALSE_NEG. PS50082; WD_REPEATS 2; 4. PS50294; WD_REPEATS_REGION; 1.

PROSITE; 1

Repeat;

REPEAT REPEAT DOMAIN

REPEAT

PROSITE;

PROSITE;

us-09-987-701-4.rsp

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1437
TVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNGQV 482
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95208357; PubMed=7900426;
Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
Yeast 10:1363-1381 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 PALDVDWQSNNTF-----ASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGN
                                                                                   363 LLASCSDDWTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNANLMLASASFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21567937; PubMed=11711434;
Pijnappel W.W.M.P., Schaft D., Roguev A., Shevchenko A., Tekotte H., Wilm M., Rigaut G., Seraphin B., Aasland R., Stewart A.F.;
"The S. cerevisiae SET3 complex includes two histone deacetylases, Hos2 and Hst1, and is a meiotic-specific repressor of the sporulation gene program.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION IN A COMPLEX WITH HOS2; HST1; SNT1; CPR1; YIL112W AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cockell M., Renauld H., Watt P., Gasser S.M.;
Sifto interacts with Sir4p amino-terminal domain and antagonizes
telomeric silencing in yeast.";
Curr. Biol. 8:787-790(1998).
                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                          1391 TVRLWSISSGKCLYTLQGHNNWVGSIVFSPDGTLLASGSDDQTVRLW----
                                                                                                                                                                                                                                                                                            01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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SIF2 OR EMBI OR YBR103W OR YBR0832.
                                                                                                                                                                                  LLNLGRSICLYTLPHHLVVIPLVA
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                                                                                                                                                                                                                                                                      STANDARD;
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CHARACTERIZATION.
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ID SIF2 YEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHESEVFICAWNPVSD-LLASGSGDSTARIWNLSENSTSGSTQ-----LVLRHCIREGG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIISMDVENVTILMNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 CSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNILASCSDDMTLKIWSMKQDNCV 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYSVAFSPDGRYLASGSFDKCVHIWNTQVCLHYLNGQVLLNLG-RSICLYTLPHHLVVIP 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSISSDEVNFLVYRYLQESGFSHSA------FTFGIKSHISQSNINGALVPPAAL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 VNLVQRGILYTESELMVDSKGDISALNEHLISEDFNLVQALQID-----KEKFFPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 SSGKTINQVICLAWSHDGNSIVTGVENGELRIWNKTGALLNVLNFHRAPIVSVKWNKXDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 PGPKGAIFVYQITEKTPIGKLIGHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 -KLDNIVSSTWNPLDESILAYGEKNSVARLARIVĖTDQEGKKYWKLTIIAELRHPFALSA
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25DD19AB2BFB4B07 CRC64;
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25.8%; Pred. No. 6.2e-27;
ive 91; Mismatches 230; Indels
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535 AA;
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Best Local Simil
Matches 140; C
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CONFLICT
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MEDLINE=21595285; PubMed=11759840; MEDLINE=21595286; Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kianko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Tabara S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8.205.213 (2001).
-!- SIMILARITY: Contains 1 NB ARC domain.
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Pfam; PF004031; NB-ARC; 1.
Pfam; PF00400; MP409; 1.
PRINTS; PR00420; GPROTEINBRPT.
PRODOM; PD000018; WD40; 1.
SWART; SN00320; WD40; 1.
PROSITE; PS50082; WD REPEATS 1; 9.
PROSITE; PS50294; WD REPEATS 2; 14.
PROSITE; PS50294; WD REPEATS REGION; 1.
HYPOCHAELICAL PSTOLIN; Repeat; Complete proteome.
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Hypothetical WD-repeat protein alr2800.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1258 AA.
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InterPro; IPR002182; NB-ARC.
InterPro; IPR001680; WD40.
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Length 1258;

DB 1;

16.9%; Score 458.5;

Query Match

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                                                                                                                                                               1020 -----TDWVYAVVFHPQGKIIATGSADCTVKLWNISTGCCLKTLSEHSDKILGMAMSPD 1073
                                                                                                                                                                                                                                                           1074 GOLLASASADOSVRLWD------ 1099
                                                                                                                                                                                                                                                                                                                                                                                                    165 LRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPS 224
                                                                                                                                        225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK 277
                                                                                                                                                                                                                   278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
                                                                                                                                                                                                                                                                                                                                                                             398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYL 457
                                                                                                                                                                                                                                                                                                 338 ODRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI
                                                                                                                                                                                                                                                                                                                                     1100 -----LRGHSNRVYSAIFSPNGEIIATCSTDQTVKIWDWQQGKCLKTLTGHTNWVFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M. Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; Intervalue;
Pfam; Pr00400; Wad0; 14;
PRINTS; PR00320; GPROTEINBRPT.
SWART; SW00320; Wad0; 14.
PROSITE; PS00672; WD_REPEATS 1; 3.
PROSITE; PS0082; WD_REPEATS 2; 14.
PROSITE; PS0294; WD_REPEATS REGION; 1.
PROSITE; PS0294; WD_REPEATS REGION; 1.
REPEAT 1070 1109 WD 1.
    32.0%; Pred. No. 1.9e-25;
tive 43; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-PEB-2003 (Rel. 41, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein all2124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1204 ASGSQDQTVRIWNVKTGECLQILRAKRL 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 ASGSFDKCVHIWN -- TQVCLHYLNGQVL 483
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MEDLINE-21595285; PubMed=11759840;
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PIR; AF2071; AF2071.
InterPro; IPR001680; WD40.
                         Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 STARIWNLSENSTSGS-TQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 ANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWN--TQVCLHYLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.5%; Score 420.5; DB 1; Length 1356; 28.2%; Pred. No. 1.2e-22; Live 63; Mismatches 164; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                         911 WD 2.
953 WD 3.
955 WD 4.
1037 WD 6.
1121 WD 6.
1120 WD 9.
1163 WD 9.
1247 WD 10.
1247 WD 10.
                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                       PEGM: PF665729; NACHT; 1.

PEMM: PF06400; WD40; 10.

PRINTS: PR00320; MP40; 10.

SWART; SW00320; WD40; 10.

SWART; SW00320; WD40; 10.

PROSITE: P550837; WG4TH; 1.

PROSITE: P550837; WD KEPEATS_1; 10.

PROSITE: P550837; WD KEPEATS_2; 10.

PROSITE: P550834; WD KEPEATS_2; 10.

GTP-binding; Repeat; WD repeat.

DOMAIN 300 307 GTP (PDENTIF)

REFEATS 339 869 WD 1.
                  SIMILARITY: Contains 10 WD repeats. SIMILARITY: Contains 1 NACHT domain.
                                                                                                                                                                    PIR; T18521; T18521.
InterPro; IPR007111; NACHT NTPase.
InterPro; IPR001680; WD40.
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ASG--TGTQT-----
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1133 11
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1217 12
1356 AA;
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Matches 117; Conserv
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"A gene responsible for vegetative incompatibility in the fungus
Podospora anserina encodes a protein with a GTP-binding motif and G
beta homologous domain.";
Gene 162.135-139 (1995).
-!- FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH
SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED GENE,
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                                                                                                                                                                                             73;
                                                                                                                                                                    Length 1683;
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                                                                                                                                         185459 MW; F7CB361FF54F7137 CRC64;
                                                                                                                                                                   DB 1;
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                                                                                                                                                                Score 451.5; DB
Pred. No. 9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 36, Created)
(Rel. 36, Last sequence update)
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incompatibility protein HET-E-1.
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1336 IIASASLDNTIRLWQRPLISPL------
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28.1%;
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Matches 123; Conservative
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15-JUL-1998
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28-FEB-2003
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218 GGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKK 277
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
WD-repeat protein HUSSY-07.
                                                                                                                                                                                                                                                                                                                                                           485 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 PPNKAVVLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIRE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 RDKLAQQQAAAAAAAAAAQQGGSAKNGENTANGE--ENGAHTIANNHTDMMEVDGDVEI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                              MEDLINE=961275.9; PubMed=8590279;
MEDLINE=961275.9; PubMed=8590279;
MEDLINE=961275.9; PubMed=8590279;
MEDLINE=961275.9; PubMed=8590279;
Surenkor A., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.,
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2.153-166(1995).
-!- SIMILARITY: Contains 16 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%; Score 394.5; DB 1; Length 1693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S76086; S76086.
InterPro; IPR008941; TPR-like.
InterPro; IPR001680; WD40.
IPR004000; WD40; 16.
PRINTS; PR00320; GPRCTEINBRPT.
PRODOM; PD000018; WD40; 13.
SMART; SM00320; WD60; 16.
PROSITE; PS00678; WD REPEATS_1; 8.
PROSITE; PS50082; WD REPEATS_2; 15.
PROSITE; PS50294; WD REPEATS_REGION; 1.
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1054 1042 WD 1.
1055 1083 WD 2.
1135 1165 WD 5.
1176 1206 WD 5.
1217 1247 WD 6.
1259 1329 WD 7.
1340 1370 WD 9.
1341 1411 WD 10.
1463 1493 WD 12.
1545 1575 WD 13.
1545 1575 WD 13.
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                                                                                                                                                      Cyanobacteria; Chroococcales; Synechocystis.
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                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical WD-repeat protein s110163.
                                                                                                                                         Synechocystis sp. (strain PCC 6803)
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1464 -----YEKNIFAAEFSADGQFIVTASDDNTAGIWEIVGREVGICRGHEGPVYFAQFSAD 1517
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                                                                                              278 GNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG 337
                                                                                                                                                                                                                                     338 ODRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTI 397
                                                                                                                                                                                                                                                                                                                                                                             398 KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL 457
                                                                                                                                                          1518 SRYİLTASVDNTARİWDF------LG
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Ninomiya K., Lwayanagi T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-21064499; PubMed=11124703;
Stanchi F., Bertocco E., Toppo S., Dioguardi R., Simionati B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1645 LTSSADGTAKLWPVKTLPQLLSQGGQWLKNY-----LTHNALVSP 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458 ASGSFDKCVHIWNTQVCLHYLN--GQVLLNLGRSICLYTLPHHLVVIP 503
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Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903(2002).
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PRINTS; PRO0319; GREOTEINB.
PRINTS; PRO0320; GREOTEINBRPT.
ProDom; PD000018; WH040; 7.
SWART; SW00320; WH040; 8.
PROSITE; PS00678; WD REPEATS_1; 4.
PROSITE; PS50294; WD REPEATS_2; 7.
PROSITE; PS50294; WD REPEATS_E2; 7.
Nuclear protein; Repeat; WD repeat.
                                                                                 446 YSVAFSPDGRYLASGSFDKCVHIW 469
                                                                                                                 460 YAVDWSPDGQRVASGGKDKCLRIW 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, BC018399, AAH18399.1, -.
InterPro, IPR001632, Gprotein_B.
InterPro, IPR001680, WD40.
Ffam, PP00400, WD40, 8
                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                   Scherl A., Coute Y., Deon C., Calle A., Kindbeiter K., Sanchez J.-C., Greco A., Hochstrasser D.F., Diaz J.-J.;
"Functional proteonic analysis of human nucleolus.";
Mol. Biol. Cell 13:4100-4109(2002)
-!- SUBCELLUIAR LOCATION: Nuclear; nucleolar.
-!- SIMILARITY: Contains 8 WD repeats.
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Cannata N., Zimbello R., Lanfranchi G., Valle G.;
"Characterization of 16 novel human genes showing high similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
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                                               yeast sequences.";
Yeast 18:69-80(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                               RC TISSUE-Lung;

RA MISDLINE-22388257; PubMed=12477932;

RA Altachul S.F., Zeeberg B. Duetow K.H., Schamen C.M., Schuler G.D.,

RA Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina R., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gap L.J., Hulyk S.W.,

RA Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Scheupers E.D., Dickson M.C.,

RA Butterfield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

RA Forc. Natl. Acad. Sci. U.S.A., 99:16899-16903 (2002).

CC --- SUBCELLUAR LOCATION: Nuclear; nucleolar (By similarity).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LISI HUMAN STANDARD; PRT; 409 AA.
P43034; Q8WZ88; Q8WZ89;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAFAH alpha) (Lissencephaly-1 protein) (LIS-1),
PAFAHIBI OR PAFAHA OR LISI OR MDCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 KLASGCKNGQILLWDPSTGLQVGRTLTGHSKWITGLSWEPLHMNPECRYVASSSKDGSVR
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=97217774; PubMed=9063735;
Lo Nigro C., Chong S.S., Smith A.C.M., Dobyns W.B., Carrozzo R.,
                                                                                                                                                                     DB 1; Length 485;
                                                                                                                                                                                                                                                       Indels
                                                                             2D7F59D603AEC07B CRC64;
                                                                                                                                                                                                                                                            48; Mismatches 145;
                                                                                                                                                                13.4%; Score 365.5; DB 1
26.6%; Pred. No. 3.2e-19;
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MEDLINE=93361119; PubMed=8355785;
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451 WI
484 WI
53148 MW;
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                                                                                                                                                                                                                                                                102; Conservative
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412
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485 AA;
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Matches 102; Conserv
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SEQUENCE FROM N.A.
TISSUE=Liver;
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Neurology 57:416-422(2001).

-!- FUNCTION: Probably involved in nuclear migration during cell division. Participates in the process of neuronal cell division. Participates in the process of neuronal cell division. Participates in the process of neuronal cell differentiation or brain development, possibly by through its role in nuclear migration of differentiating neurons. May participate in nargeting cytoplasmic dynain to the microtubule plus ends, thereby playing an essential role in dynein-mediated microtubule sliding. Non-catalytic subunit of a acetylhydrolase complex, a complex that inactivates platelet-activating factor (PAF) by removing the acetyl group at the SN-2 position.

-!- SUBUNT: Cytosolic PAF-AH IB is formed of three subunits of 45 kDa (alpha), 30 kDa (beta) and 29 kDa (gamma). The catalytic activity of the enzyme resides in the beta and gamma subunits, whereas the alpha subunit has regulatory activity. Trimer formation is not essential for the catalytic activity. Interacts with dynein and dynactin. Interacts with RSN.

-!- SUBCELLULAR LOCATION: Cytoplasmic, localizes to the plus end of
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20512525; PubMed=11056532;
Faulkner N.E., Dujardin D.L., Tai C.-Y., Vaughan K.T., O'Connell C.B.,
Wang Y.-L., Vallee R.B.;
"A role for the lissencephaly gene LIS1 in mitosis and cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microtubules.
TISSUE SPECIFICITY: Fairly ubiquitous expression in both the frontal and occipital areas of the brain.
DISEASE: Defects in PARAHIB1 are the cause of classical lissencephaly-1 (LIS1) [MIM:607432]. LIS1 is a brain malformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT SBH PRO-168.
MEDIINE=99371784; Pubmed=10441340;
MEDIINE=99371784; Pubmed=10441340;
Pilz D.T., Xuo J., Matsumoto N., Bodurtha J., Bernadi B.,
Passinari C.A., Jobyns W.B., Ledbetter D.H.;
"Subcortical band heterotopia in rare affected males can be caused by missense mutations in DCX (XLIS) or LIS1.";
Hum. Mol. Genet. 8:1757-1760(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=21938534; PubMed=11940666; Coquelle F.M., Caspi M., Cordelieres F.P., Dompierre J.P., Coquelle F.M., Caspi M., Cordelieres F.P., Dompierre J.P., Milmanova A., Galjardin D.L., Koifman C., Martin P., Hoogenraad C.C., Akhmanova A., Galjart N., De Mey J.R., Reiner O., Ellis, Chip-170's key to the dynein/dynactin pathway."; Mol. Cell. Biol. 22:3089-3102(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS LISI SER-30; SER-161 AND HIS-316.
MEDLINE-21394321; PubMed=11502906;
Leventer R.<sup>2</sup>., Cardoso C., Leddbetter D.H., Dobyns W.B.;
List missense mutations cause milder lissencephaly phenotypes including a child with normal 10.";
                                                                                                                                                                                                                                                  TISSUE-Colon; Webner D., Mewes H.-W., Weil B., Amid C., Osanger Wambutt R., Heubner D., Memes H.-W., Weil B., Wiem M., Wiemann S.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION, AND INTERACTION WITH DYNEIN AND DYNACTING
Zhao M.J., Xia S.L., Li T.P.; "High expression of the lissencephaly gene in hepatocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21898370; PubMed=11889140;
Tai C.-Y., Dujazdin D.L., Faulkner N.E., Vallee R.B.;
"Role of dynein, dynactin, and CLIP-170 interactions in LIS1 kinetochore function.";
                                                          patients.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                          Feng Z., Zhang B., Peng X., Yuan J., Qiang B., submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION, AND INTERACTION WITH RSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH RSN; DYNEIN AND DYNACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dynein function.";
Nat. Cell Biol. 2:784-791(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Biol. 156:959-968(2002).
                                                                                                                           SEQUENCE FROM N.A.
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CONFLICT
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DISBASE: Defects in PARAHIBI are a cause of Miller-Dieker

DISBASE: Defects in PARAHIBI are a cause of Miller-Dieker

Lissencephaly syndrome (MDLS) [MIM:247200]. MDLS is a form of

Lissencephaly associated with facial abnormalities.

SIMILARITY: Contains 1 LisH domain.

SIMILARITY: Contains 7 WD repeats.

CAUTION: Ref. 1 (AAA02882) sequence differs from that shown due to

CAUTION: Ref. Is sequence differs from that shown due to what seems

to be the presence of intronic sequence in the CDNA.

DATABASE: NAME=HotMolecBase; NOTE=LISI entry;

WWW="http://bioinformatics.weizmann.ac.il/hotmolecbase/entries/lis1.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
caused by abnormal neuronal migration at 9 to 13 weeks' gestation. Lissencephaly means 'smooth brain', a brain without convolutions or gyri, and consists in an absence (agyria) or a decrease (pachygyria) of surface convolutions associated with a disorganization of the clear neuronal lamination of normal sixlayered cortex. It is characterized by an abnormally thick and poorly organized cortex with 4 primitive layers, diffuse neuronal heterotopia, enlarged and dysmorphic ventricles, and often hypoplasia of the corpus callosum.

-!- DISEASE: Defects in PARAHIBI are the cause of subcortical band heterotopia (SBH) [MIN:607432]. SBH is at the less severe end of the lissencephaly spectrum of malformations, characterized by bilateral and symmetric ribbons of gray matter found in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, L13385, AAA02880.1;
EMBL, L13386, AAA02881.1;
EMBL, U13347, AAA02881.1;
EMBL, U7342; AAC5111.1;
EMBL, U7234, AAC5111.1;
EMBL, U72335, AAC5111.1;
U72336, AAC5111.1;
U72336, AAC5111.1;
U72336, AAC5111.1;
U7231, AAC5111.1;
U7231, AAC5111.1;
U7231, AAC5111.1;
U7231, AAC5111.1;
U7231, U72339, AAC5111.1;
U7231, U72341, AAC5111.1;
U72341, AAC5111.1;
U72341, AAC5111.1;
EMBL, AF20883, AAC5111.1;
EMBL, AF20883, AAC5111.1;
EMBL, AF40843;
EMBL, AAC5111.1;
EMBL, AAC0838;
EMBL, AAC0838;
EMBL, AAC0838;
EMBL, AAC0838;
EMBL, AAC0838;
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EMBL, AAC0888;
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126 NGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 EW------IPRPPEK-YALSGHRSPVTRVIFHPVFSVMV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SASEDATIKVWDYETGDFERTLKGHTDSV------QDI-----SFDHSGKLLA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 TGSYDGFARIWTKDG-NLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GNILLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP-----TGPGT-NNP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 GTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPESSYSSISEATGSETKKSG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 -----VKTFTGHREWVRMVRPNQD 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 DEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYVEAEVS 65
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D LISH BOVIN STANDARD; PRT; 409 AA.

D LISH BOVIN STANDARD; PRT; 409 AA.

D LISH BOVIN STANDARD; PRT; 409 AA.

D LISH STANDARD; Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 00-COT-2003 (Rel. 42, Last sequence update)

DF 10-COT-2003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 SGSGDSTARIWNLS----ENSTSGSTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLA
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                                        COILED COIL (POTENTIAL).
                                                                             WD 1.

WD 2.

WD 3.

WD 4.

WD 5.

WD 5.

WD 7.

FTIGAVAR 015398.

H -> R (in LIS1).

FTIGAVAR 01739.

G -> S (in LIS1).

FTIGAVAR 01739.

S -> P (in ES1).

FTIGAVAR 01539.

FTIGAVAR 01539.

FTIGAVAR 01539.

FTIGAVAR 01539.

FTIGAVAR 01539.

S -> P (in LIS1).

FTIGAVAR 01539.

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S -> P (in LIS1).

FTIGAVAR 01539.

FTIGAVAR 01539.

S -> P (in LIS1).

FTIGAVAR 01539.
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Matches 109; Conservative
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                                                                                                                                                                                                                               Nature 370.216-218 (1994).

Nature 370.216-218 (1994).

1. Nature 370.216-218 (1994).

1. division. Participates in the process of neuronal cell
division. Participates in the process of neuronal cell
division. Participates in the process of neuronal cell
division. Participates on the process of neuronal cell
differentiation of differentiating neurons. May participate
in nuclear migration of differentiating neurons. May participate
in targeting cytoplasmic dynean to the microtubule plus ends,
thereby playing an essential role in dynein-mediated microtubule
sliding. Non-catalytic subunit of a acetylhydrolase complex, a
complex that inactivates platelet-activating factor (PAP) by
removing the acetyl group at the SN-2 position (By similarity).

SUBUNITY: Cytosolic PAP-AH IS is formed of three subunits of 45 kDa
(alpha), 30 kDa (beta) and gamma subunits, whereas the
alpha subunit has regulatory activity. Trimer formation is not
essential for the catalytic activity. Interacts with dynein and
dynactin. Interacts with RSN (By similarity).

--- SUBCELUTAR LOCATION: Cytoplasmic, localizes to the plus end of
microtubules (By similarity).

--- SIMILARITY: Contains 7 WD repeats.
Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0896; LISH; 1.
PROSITE; PSS0896; MD REPEARS 1; 4.
PROSITE; PSS0082; WD REPEARS 2; 7.
PROSITE; PSS0094; WD REPEARS 2; 7.
PROSITE; PSS0294; WD REPEARS REGION; 1.
Call division; Mitosis; Neurogenesis; Cytoskeleton; Microtubule;
Repeat; Coiled coil; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 409;
                                                                                                                                                              Hattori M., Adachi H., Tsujimoto M., Arai H., Inoue K., "Miller-Dieker lissencephaly gene encodes a subunit of brain platelet-activating factor acetylhydrolase.";
Nature 370:216-2218(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6EECF9F71D2F182F CRC64;
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COLLED COIL (POTENTIAL).
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WD 5.
WD 7.
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                                                                                                  [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                MEDLINE=94301405; PubMed=8028668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D30615; BAA06305.1; -.
InterPro; IPR001680; W140.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00657; Lish; 1.
SMART; SM00320; WD40; 7.
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261
365
                                                         Bovidae; Bovinae; Bos.
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Best Local
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410 NANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIW 469
                                                                                                                                                                                                                                                       TGSYDGFARIWTKDG-NLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA 300
                                                                                                                                                                                                                                                                                                                               801 KQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIKWDPT 360
                                                                                                                                                                                                                                                                                                                                                                                                    GNILLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSP------TGPGT-NNP 409
                                                                                                                                                                                                                                                                                                                                                                                                                           126 NGENTANGEENGAHTIANNHIDMMEVDGDVEIPPNKAVVLRGHESEVFICAWNPVSDLLA 185
                                                                                                                                             -----IPRPPEK-YALSGHRSPVTRVIFHPVFSVMV 123
                                                                                                                                                                               SGSGDSTARIWNLS----ENSTSGSTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLA 241
                                                                                                                                                                                                                                                                                -----YC----VKTFTGHREWVRPNOD 244
--AAYSVFKK----EAELD 37
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MEDIANE-22388257; PubMed=12477932;

MEDIANE-22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shanmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz I.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P.,

Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shi Y.;
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Adams M.D., Loftus B.J., Zhou L., Crosby M., Fuhrmann J., Mason T.M.,
Brandon R., Kim U.J., Kerlavage A.R., Venter J.C.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                  66 INEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAAAAAX
                                                                     38 MNEE---LDKK---YAGLLEKKWTSVIRLOKKVMELESKLNEAKEEFTSGGPLGOKRDPK
                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Johnstone R.W., Wang J., Tommerup N., Vissing H., Roberts T.,
"Ciao 1 is a novel WBdo protein that interacts with the tumor
suppressor protein WT1.";
J. Biol. Chem. 273:10880-10887(1998).
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15-MAR-2004 (Rel. 43, Last annotation update)
WD-repeat containing protein Ciao 1.
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076071;
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14; 65

Indels 141; Gaps

Matches 108; Conservative

Similarity

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30; GO:0008284; P:positive regulation of cell proliferation; TAS.
30; GO:0006357; P:regulation of transcription from Pol II pro. .; TAS.
InterPro; IPR001680; WD40.
Pfam; PP00400; WD40.
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahelton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., "Generrh A., Schein J.E., Jones S.J.W., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                 Length 339;
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                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 2.6e-18;
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PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
Repeat; WD repeat; Nuclear protein.
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289 WD
338 WD
37840 MW;
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PRINTS; PR00320; GPROTEINBRPT.
PRODOM; PD000018; WD40; 2.
SMART; SM00320; W440; 7.
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31.9%;
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Best Local Similarity 31.9'
Matches 86; Conservative
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LGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDN---CVHDLQQHNK 392

336

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152 DVKHVVWHP-----SQELLASASYDDTVKLYREEEDDWVCCATLEGHESTVWSLAF 202
                                              393 EIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLW--DVDRGICIHTLTKHOEPVYSVAF 450
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Search completed: August 9, 2004, 16:46:12 Job time : 10.6667 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 9, 2004, 16:41:13; Search time 34.6667 Seconds (without alignments) 4678.164 Million cell updates/sec Run on:

US-09-987-701-4 2718 Title: Perfect score) Sequence:

1 MSISSDEVNFLVYRYLQESG......LPHHLVVIPLVALIELLVLK 514

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 segs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL 25:* Database :

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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ALIGNMENTS

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SEQUENCE 2534683; PubMed=12466831;

TATALINE-2534683; PubMed=12466831;

The FANTOM Consortium,

The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The Go, 770 full-length cDNAs.";

The Go, 770 full-length cDNAs.";

The Malysis of the mouse transcriptome based on functional annotation of Nature 420:563-573(2002).

The REBL; AK023547; BAC26261;

REBL; AK033347; BAC26261;

REBL; AK033347; BAC26241.1;

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REBL; AK033847; BAC28241.1;

REBL; AK033847; BAC681.

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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01-OCT-2003 (TrEMBLrel, 25, Last ann
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X MEDLINE-2354663; PubMed=1246681;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team,
The RIKEN Genome Exploration Research Group Phase I & II Team,
T "Analysis of the mouse transcriptome based on functional annotation of
T 0,770 full-length CDNAs.";
The Malysis of the mouse transcriptome based on functional annotation of
T 0,770 full-length CDNAs.";
The AZO:563-573(2002).
R PEMB: ARO:563-573(2002).
R MGD; MGI:2441730; Irai.
R MGD; MGD:40651; DISH.
R MGD; MGD:40650; MP40. 8.
R PRINTS; PRO01600; WD40. 8.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Query Match 90.8%; Score 2468; DB 11; Length 514; Best Local Similarity 98.5%; Pred. No. 5e-167; Matches 465; Conservative 2; Mismatches 5; Indels 0
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
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IRA1 OR 8030499H02RIK.
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                                                                                                                                             1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYV 60
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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                                              Query Match 90.7%; Score 2465; DB 11; Length 514; Best Local Similarity 98.3%; Pred. No. 8.2e-167; Matches 464; Conservative 3; Mismatches 5; Indels 0;
514 AA; 55689 MW; 13BED3753A725029 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS0678; WD REPEATS_1; 4.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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SMART; SM00320; WD40; 8.
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MEDLINE-22388257; PubMed=12477932;

REALINE-22388257; PubMed=12477932;

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RELINE-22388257; PubMed=12477932;

RELINE-22388257; PubMed=12477932;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buercw K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Saares M.B., Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Rosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.N., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.N., Gabs R.A.,

Rahesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rational M. M. I., Skalska U., Smailus D.E., Schnerch A., Scheln J.B.,

"Generation and initial analysis of more than 15,000 full-length human
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       BAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQAAAAAAAAAA-- 118
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STRAIN=CS7BL/60; TISSUE=Hypothalamus;
STRAIN=22354683; Pubmed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                              ASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                           AWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGODVPSNKDVTSLDWNS
                                                                               ---SQQGSAKNGENTANGEENGAHTIANNHIDMMEVDGDVEIPPNXAVVLRGHESEVFIC
                                                                                                    121 TPNNQQPPAKNGENTANGESNGGHALANNHTDMMEVDGDVEIPSSKAVVLRGHESEVFIC
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Transducin (Tbllx protein)
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Mammalia; Eutheria;
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                                                                                                                                             1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
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                                                                           Gaps
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"Fusion Protein of Retinoic Acid Receptor falpha} with Promyelocytic
Leukemia Protein or Promyelocytic Leukemia Zinc Finger Protein
Recruits N-CoR-TBLRI Corepressor Complex to Repress Transcription in
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nuclear receptor co-repassor complex subunit TBLR1.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Pred. No. 1e-163;
4; Mismatches 10; Indels
 6A72CE68A40C141F CRC64;
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                                      DB 11;
                                    tch
al Similarity 98.3%; Pred. No. 9.6e-167
464; Conservative 2; Mismatches 6
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EMBL; AY225088; AAP20646.1; -.
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 55689 MW;
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96.0%;
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514 AA;
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J. Biol.
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
       cDNA sequences.";
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Pituitary;

MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the wouse transcriptome based on functional annotation of

"G0,770 full-length cDNAs.";

IN The FANTOM Consortium,

Nature 420:563-573(2002).

IN MALL AKOS1847; BAC27015.1;

R MGD; MGI:1336172; Tblix.

R MGD; MGI:1336172; Tblix.

R InterPro; IPRO06584; List.

R InterPro; IPRO06584; List.

R InterPro; IPRO01680; WA40.

R Pfam; PF00400; WA40.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.2%; Pred. No. 6.6e-153;
Matches 424; Conservative 26; Mismatches 21; Indels 15;
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PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 1; 4.
PROSITE; PS50094; WD REPEATS REGION; 1.
SEQUENCE 527 AA; 56832 MW; 0466F764ABA25CB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0120; GPROTEINBRPT.
PRODON; PD0000018; WD40; 3.
SMART; SM0067; LisH; 1.
SMART; SM00320; WD40; 8.
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RESULT Q86UY2

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(TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                             468 IWNTQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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01-OCT-2003
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RA Strauberg R.L., Felngold B.A., Grouse L.H., Derge J.G.,

RA Strauberg R.L., Felngold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Widin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.S., McZwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

R. Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Villalon D.K., Muany D.M., Sodergren E.J., bu X., Gibbs R.A.,

R. Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R. Rodriguez A.C., Grimwood U., Smailus D.E., Schnerch A., Schein J.B.,

Jones S.J., Marra M.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Warra R.A.,

R. Jones S.J., Marra M.A.,

R. Jones S.J., Warra R.A.,

R. Jones S.J., Warra R.A.,

R. Jones S.J., Warra M.A.,

R. Jones J.J., Warra M.A.,

R. Jones J.J., Warra M.A.,

R. Jones J.J., Warra M.A.,

R. Jones J.J., Warra 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 HESEVFICAWNFVSDLLASGSGDSTARIWNINENSNGGSTQLVLRHCIREGGHDVPSNXD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Indels 14; Gaps
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC052304; AH522904.1; -.
InterPro; IPR005694; LisH.
InterPro; IPR005694; WD40.
Pfam; PF00400; WD40; 8.
PRINTS; PR00320; WD40; 3.
SMART; SM00567; LisH; 1.
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PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50294; WD REPEATS REGION; 1.
SEQUENCE 577 AA; 62495 NW; D830A37781E2A1SC CRC64;
                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.0%; Score 2229; DB 4; Best Local Similarity 85.4%; Pred. No. 5.6e-150; Matches 414; Conservative 32; Mismatches 25;
     577 AA
                                         Created)
                             01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                     TBL1X protein.
Homo sapiens (Human)
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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228 VTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVD 287
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STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINB=2234683; PubMed=12466851;
The FANTOM COnsortium.
The FANTOM Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Mature 420:565-573(2002).
                        288 KITIIWDAHIGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHYCKLGQDRPIKTFQG
                                                                                                                 351 KTTIINDAHTGEAKQOPPHSAPALDVDWQNNTTFASCSTDMCIHVCRLGCDRPVKTPOG
                                                                                                                                                                     348 HTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTN
                                                                                                                                                                                                NPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 VLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATATSTAATTPAAAAQQNPPKNGEATVNGEENGAHAI-NNHSKPWEIDGDVEIPPSKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 VLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AQQQAAAAAAAAAAAQQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPPNKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8e-117;
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64.8%; Score 1761.5;
Best Local Similarity 87.0%; Pred. No. 5.8e
Matches 321; Conservative 20; Mismatches
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RXATK=Resteley,
RXATK=Resteley,
RXATK=Resteley,
RAMEDLINE=20196006, PubMed=10731132,
RADINE=20196006, RADINE=20196, RADINE=2019600, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=20196006, RADINE=201
                                                                                                                                                                                                            302 PATSNPNSNIMLASASFDSTVRLWDVERGVCIHTLITKHQEPVYSVAFSPDGKYLASGSFD 361
284 AGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIK 343
                        182 AGVDKTTIIMDAHTGEAKQOPPFHSAPALDVDWQNNTTFASCSTDMCIHVCRHGCDRPVK 241
                                                                                            344 TFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTG 403
                                                                                                                     404 PCTNNPNANLMLASASFDSTVRLWDVDRGICIHTLIKHQEPVYSVAFSPDGRYLASGSFD 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBI protein.

EBI OR CG4063.

Drosophila melanogaster (Fruit fly).

Brwaryota; Merazca; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoprera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                               464 KCVHIWNTQ 472
                                                                                                                                                                                                                                                                                                                            362 KCVHIWNTO 370
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Q9XZK1
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A CELLIKER S.E., George R.A., Galle R.F., Hoskins R.A., Svirskas R.R.,

RA Harris N.L., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

Canavez C., Chew M., Doyle C.M., Farfan D.E., Flanagan J.,

A Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim S.H., Lee B.,

Ra Lomotan M.A., Mak J., Mazda P., Moshrefi A.R., Moshrefi M., Nixon. K.,

Ra Lomotan M.A., Mak J., Parel E., Snir E., Twomey B.,

RA WAN K.H., Zhang R., Zlezan L.I., Rubin G.M.;

REBL, Acto3589; AAF51501.1; -.

BRBL; Act05782; -. NOT the EMBL/GenBank/DDBJ databases.

BRBL; Act06782; -. NOT ANNOTATED CDS.

REBL; Act06782; -. NOT ANNOTATED CDS.

REBL; Act06589; MAP DIA.

RICEPPO; IRRO06599; Myb DNA, Dinding.

RICEPPO; IRRO06599; Myb DNA, Dinding.

RICEPPO; IRRO06599; Myb DNA, Dinding.

RICEPPO; IRRO06599; Myb DNA, Dinding.

RICEPPO; IRRO06599; Myb DNA, Dinding.

READ: PROSUTE; PRO01018; WD40; 8.

RRAT; SM00320; GRRCTEINBRPT.

BROOGOTS; WD40; 8.

RRAT; SM00320; WD40; 8.

RROSITE; PS00678; WD REPEATS 2; 6.

BROSITE; PS0082; WD REPEATS 2; 6.

BROSITE; PS0082; WD REPEATS 2; 6.

BROSITE; PS0082; WD REPEATS 2; 6.

BROSITE; PS0082; WD REPEATS 2; 6.

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BROSITE; PS0082; WD REPEATS 2; 6.

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BROSITE; PS0082; WD REPEATS 2; 6.

BROSITE; PS0082; WD REPEATS 2; 6.

BROSITE; PS0082; WD REPEATS 2; 6.

BROSITE; PS0082; WD REPEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDÓSASEVDSSGNAANNAGGTYAGNNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 AGGNQASTGGSNSTSTPAGGDLAAPCASOKKSONSNEAGSSSSGNAGNANATSTDDAASS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 TSTNGNSSTSSSVEQPTSGLTPAGGTVSTSNPDAAASGGASTATGSKAPSGAVTIRVGAQ 298
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                                                                                                                                           "ebi regulates epidermal growth factor receptor signaling pathways in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.1%; Score 1715.5; DB 5; Length 700; Best Local Similarity 52.9%; Pred. No. 2.38-113; Matches 71; Indels 191; Gaps Matches 349; Conservative 49; Mismatches 71; Indels 191; Gaps
                         SEQUENCE FROM N.A.
DEDLINE=99234084; PubMed=10215623;
DONG X., Tsuda L., Zavitz K.H., Lin M., li S., Carthew R.W., Zipursky S.L.;
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                                                                                                                                                                                                 Genes Dev. 13:954-965(1999).
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233 WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII 292

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WDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV 352
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                                                                                                      LMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Haysshizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                     NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKEIYTIKWSPTGPGTNNPNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana chromosome 5. III.
1,191,918 bp covered by seventeen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.
                                                                                                                                                                                                                                                                                                                                                                                                               E., Miyajima
                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-07-2003 (TrEMBLrel. 25, Last annotation update)
Genomic DNA, chromosome 5, TAC clone: K8K14 (AT5g67320/K8K14_4).
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Arabidopsis ORF clones.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB007645; BAB09017.1; -.
EMBL; AY057698; AAL15328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98162728, PubMed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu
                                                                                                                                                                                                                           613
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Sequence features of the regions of
physically assigned P1 clones.";
DNA Res. 4:401-414(1997).
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InterPro; IRR006594; Lish.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
PRINTS; PR00320; GPROTEINBRPT.
SWART; SM00320; WD40; 2.
SWART; SM00320; WD40; 8.
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SEQUENCE FROM N.A.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 ASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAKQQFPFHSAPALDVDWQS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 ISTLSKHKGPIFSLKWNKKGDYLLTGSVDRTAVVWDVKABEBWKQQFEFHSGPTLDVDWRN 417
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                                                                                                                                                                                                                                                                                                                                         SISSDEVNFLVYRYLQESGFSHSAFTFGIKSHISQSNINGALVPPAALISIIQKGLQYVE
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
                                                                                                                                                                                                                                                                                  Indels 108;
                                                                                                                                                                                                                           DB 10; Length 613;
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Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bohydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                    04F40772311C0E76 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                        / Match 46.0%; Score 1251; DB 10; Local Similarity 43.4%; Pred. No. 1.9e-80; Hes 248; Conservative 85; Mismatches 131;
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PROSITE, PS00678; WD REPEATS_1; 3.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
REPAGA; WD TEPEATS_REGION; 1.
SEQUENCE 613 DA.
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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SEQUENCE FROM N.A.
   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 NAKPEIKIEPGTGVAGSÅGGNKIÅGSTTGTSTPTDÖSÅSEVDSSGNAANNAGGTYAGNNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 AGGNQASTGGSNSTSTPAGGDLAAPGASQKKSQNSNBAGSSSSGNAGNANATSTDDAASS 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 14.0%; Score 923.5; DB 5; Length 524; Local Similarity 40.5%; Pred. No. 2.8e-57; Los 218; Conservative 39; Mismatches 64; Indels 217; Gaps
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01-WAR-2002 (TrEWBLrel. 20, Last sequence update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Similar to IRAI protein (Fregment).
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, AYOGA326, AAL280874.1;
FIYBASE, FEBRO003344; ebi.
R GO: GO:000074; P:regulation of cell cycle; IMP.
R InterPro; IPR001065; Mbd.
R InterPro; IPR001065; Mbd.
R InterPro; IPR001065; Mbd.
R FINTS; PR00320; MD40.3.
R PRINTS; PR00300; MD40.1.
R SWART; SM00667; Lish; 1.
R SWART; SM00367; MD40; 3.
R PROSITE; PS00037; MP2 1; 1.
R PROSITE; PS00037; MP2 1; 1.
R PROSITE; PS00037; MD2 1; 1.
R PROSITE; PS00037; MD2 1; 1.
R PROSITE; PS00037; MD REPEATS 1; 2.
R PROSITE; PS00047; WD REPEATS 2; 3.
R PROSITE; PS00047; WD REPEATS 2; 3.
R PROSITE; PS00047; WD REPEATS 2; 3.
R PROSITE; PS00047; WD REPEATS 2; 3.
R PROSITE; PS00047; WD REPEATS 2; 3.
R PROSITE; PS00047; WD REPEATS 2; 3.
R PROSITE; PS00057; WD REPEATS 2; 3.
R PROSITE; PS00057; WD REPEATS 2; 3.
R PROSITE; PS00057; WD REPEATS 2; 3.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Maranbe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Rishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Rishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M.,
Rasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M.,
RA Sasuda M., Tabata S.,
Complete genomic sequence of the filamentcus nitrogen-fixing
RT Cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 81.205-213(2001).
BRI, AP003581; BAB77553.1; -.
DR REL; AP003581; BAB77553.1; -.
DR RO, GO.0005524; F.ATP binding; IEA.
GO; GO.0005524; F.ATP binding; IEA.
GO; GO.0005524; F.ATP binding; IEA.
GO; GO.0005525; P. Laranscription factor activity; IEA.
GO; GO.0006315; P. Papoptosis; IEA.
GO; GO.0006315; P. Pregulation of transcription, DNA-dependent; IEA.
DR GO; GO.000535; P. Pregulation of transcription, DNA-dependent; IEA.
BR InterPro; IPR00197; HTH Fis.
BR InterPro; IPR00197; HTH Fis.
BR InterPro; IPR00182; MP40.
BR InterPro; IPR00182; MP40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          314 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNBVNAIKWDPTGNLLASCSDDMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTL
                                                                                                                                                                                                                                                                                                                                                                                              Gabs
                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                          32.5%; Score 882; DB 11; Length 201; 99.4%; Pred. No. 6.5e-55; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                   SEQUENCE 201 AA; 22038 MW; 6B945F137B491818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 CIHTLIKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
WD-40 repeat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1227 AA.
Strausberg R.;
Submitted (DEC_2001) to the EMBL/GenBank/D
EMBL; BC018512; AAH18512.1;
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 4.
PRINTS; PR00320; GFROTEINBRPT.
ProDom; PD000018; WD40; 2.
SWART; SW00320; WD40; 4.
PROSITE; PS00678; WD REPEATS 1; 2.
PROSITE; PS00678; WD REPEATS 2; 3.
PROSITE; PS00678; WD REPEATS 2; 3.
PROSITE; PS0082; WD REPEATS 2; 3.
PROSITE; PS0082; WD REPEATS 2; 3.
PROSITE; PS0082; WD REPEATS 2; 3.
PROSITE; PS0082; WD REPEATS 2; 3.
PROSITE; PS0082; WD REPEATS 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 99.4
Matches 158; Conservative
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PRT; 1356
                                                                                                                                    PROSITE; PSS0837; NACHT; 1.
PROSITE; PSS0837; NACHT; 1.
PROSITE; PSS06082; WD_REPEATS_1; 10.
PROSITE; PSS0294; WD_REPEATS_REGION; 1.
Repeat; WD_repeat.
SEQUENCE 1356 AA; 149694 WW; 572A0B
                                    PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 10.
SMART; SM00320; WD40; 10.
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   Pfam; PF00400; WD40; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 ASQQGSAK----NGE--NTANGEENGAHTIANNHTDMMEVDG-------DV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 834 CGEDRSIKLWDIORGECVNTLWCHSSQVWAIA-----FSPDGRTLISCSDDQTARLWDV 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 LKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQ-SNNTFASCSTDMC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 IHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQH 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 EIPPNKAVVLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                888 - ITGNSLNILKGYTRDVYSVAFSPDSQILASGRDDYTIGLWNLKTGEC------HPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 NKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTK-HQEPVYSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 16.4%; Score 444.5; DB 16; Length 1227; 29.2%; Pred. No. 9.9e-23; ive 73; Mismatches 171; Indels 71;
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Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
VCBI_TaxID=5145;
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"A new family of WD40 proteins implicated in vegetative incompatibility; evidence for a major role of WD40 repeat the specificity of het-e and het-d genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF332584; AAL37300.1;
InterPro; IPRO07111; NACHT_NTPase.
InterPro; IPRO07111; NACHT_NTPase.
Figure PF05729; NACHT; 1.
                                                                                                                                                                                                                                                                                                                                                   1227 AA; 137236 MW; 466F726939ED4FBF CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*40.
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                                                                                                                             SMART; SM00320; WD40; 14.
TIGRPAMS; TIGRO1199; HTH fis; 1.
PROSITE; PS00678; WD REPEATS 1; 12.
PROSITE; PS50082; WD REPEATS 2; 14.
PROSITE; PS50294; WD REPEATS REGION; 1.
COMDISTE DESCREAMS REGION; 1.
SEQUENCE 1227 AA; 137236 MW; 466F72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1163 FSPDGRLLASGSEDEKIQLWDMQNC 1187
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                             PRINTS; PR00364; DISEASERSIST PRINTS; PR00320; GPROTEINBRPT ProDom; PD000018; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lòcal Similarity 29.23
1es 130; Conservative
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WD40; 14
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1120 WDAASGTCTQTLEGHGDSVWSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEGHGGW 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 VVLRGHESEVFICAMNPVSDLLASGSGDSTARIWNLSENSTSGS-TQLVLRHCIREGGQD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 ILSAGVDKITIIWDAHIGEAKQQFPFHSAPALDVDWQSNNTF-----ASCSTDMCIHV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 CKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQQHNKE 393
                                                                                                                                                                                                                                        56 GLQYVEA-----EVSINEDG-TLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD
                                                                                                                                                                                                                                                                                109 AAAAAAAAAAQQGSAKNGE-----NTANGEENGAHTIANNHTDMMEVDGDVEIPPNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Espagne E., Balhadere P., Begueret J., Turcq B.;
"A new family of W040 proteins implicated in vegetative
incompatibility; evidence for a major role of W040 repeat domain in
the specificity of het-e and het-d genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF333582; AA1372881, -1.
InterPro; IPR00111; NACHI_NTPase.
InterPro; IPR00160; W040.
Pfam; PF00400; W040: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                            | : | : | : | : | 927 SVLSVAFSPDGQRVASGSGDKTIKIWDTASG--TGTQT---------
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1231 GORVASGSSDNTIKIWDTASGTCTQTLNVGSTATCLSFDYTNAYINTNIGR 1281
                                                                                            Query Match
16.3%; Score 442; DB 3; Length 1356;
Best Local Similarity 27.6%; Pred. No. 1.7e-22;
Matches 130; Conservative 71; Mismatches 168; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 GRYLASGSFDKCVHIW------NTQVCL--HYLNGQVLLNLGR
repeat.
1356 AA; 149694 MW; 572A0B034DCE0D21 CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C.
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1066 VASGSIDGTIKIWDAASGTCTQTLEGHG-----DWVQSVAFSPDGQRVASGSDDHTIKI 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD 453
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Best Local Similarity 27.6%; Pred. No. 1.7e-22;
Matches 130; Conservative 71; Mismatches 168; Indels 102; Gaps
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DE PEODOM; PD000018; WD40; 10.

R SMART; SW00320; WD40; 10.

R PROSITE; PS50837; NACHT; 1.

R PROSITE; PS50837; WD REPEARS 1; 10.

R PROSITE; PS50082; WD REPEARS 2; 10.

R PROSITE; PS50294; WD REPEARS 2; 10.

R REPEAR; WD repeat.

R REPEARS REGION; 1.
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Search completed: August 9, 2004, 16:48:10 Job time: 47.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 9, 2004, 16:41:43; Search time 13.333 Seconds (without alignments) 3708.183 Million cell updates/sec Run on:

US-09-987-701-12
2731
1 MSISSDEVNFLVYRYLQESG.....GDKVGASASDGSVCVLDLRK 514 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283366 segs, 96191526 residues Searched:

283366

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0	& Query		6	S OMMAKI ES	
l ke	Match	Length	8	qi	Description
501.5			7	N	probable membrane
81	۲.	Н	0	AC2239	WD-40 repeat prote
62	16.9	П	7	T18521	transducin-l
s.		П	~1	A12155	WD-repeat protein
51	Ġ.	М	7	AF2071	
137	•	Н	7	AE1810	-40 repeat prot
.5	16.0	П	7	AI2493	-repeat pro
7.	16.0	_	~	AE1866	repe
115	15.2	-	7	AD1842	
.5	14.8		(1	AC1842 \	-40 repeat prot
3.	4			AG1889) repeat
1.5	4		7	T40883	Ω
.5	14.3	_	~	876086	beta transducin-li
85.5	14.1		7	AH2195	hypothetical prote
385	14.1	-	0	AB2410	WD-repeat protein
ιú	13.7		(7	S19487	hypothetical prote
173	13.7	7	7	AH2154	WD-repeat protein
ŗ.	13.5		7	T41148	trp-asp repeat con
	13.4		7	AG1837	WD-40 repeat prote
362	13.3		7	AF1890	WD-repeat protein
358	13.1		~	S05357	hypothetical prote
'n.	12.9		~	AE1861	serine/threonine k
5	12.6		N	AG2375	WD-40 repeat-prote
340	12.4		N	G85034	probable WD-repeat
.5	$^{\circ}$	559	7	AB2202	hypothetical prote
5.	12.2	410	7	5	-H
331	ď.	323	7	T02617	_
31	12.1	777	~	0	hypothetical WD-re
.5	12.1	409	N	3611	Ë

PP20 protein, micr WD-repeat protein hypotherical prote	hypothetical prote hypothetical prote WD-repeat protein METAL Protein - ve	WD-40 repeat prote hypotherical prote beta transducin-li WD-40 repeat regul	beta transducin-li transcription init transcription init hypothetical prote
T08180 AG2400 T33805	T00798 T22703 AE2490 S49932	A12099 T19266 T42045 T46032	S76414 S33263 T41454 T27513
0000	10000	0000	0 0 0 0
606 589 473	787 787 342 640	357 376 1049 317	1191 704 643 501
122.0		111111111111111111111111111111111111111	11.4 11.3 11.2 11.2
328.5 328 327.5	325.5 324.5 324 313	312 312 312 311.5	310 307.5 307 303.5
321	8 8 8 8 4 8 9 7	8 8 8 9 4 4	4 4 4 4 2 6 4 8

ALIGNMENTS

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A12155
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Dostoc sp. PCC 7120
C;Species: Ostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: A12155
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
                                                                                                                                                                           Detair transducin-like protein - Podospora anserina
C;Species: Podospora anserina
C;Species: Podospora anserina
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18521
R;Saupe, S.; Turoq, B.; Begueret, J.
Gene 162, 135-139, 1995
A;Title: A gene responsible for vegetative incompatibility in the fungus Podospora anseri
A;Reference number: 218944; MUID:96009891; PMID:7557402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1393 RLWSISSGKCLYTLQGHNNWVGSIVFSPDGTLLASGSDDQTVRLWNISSGECLYTLHGHI 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IESLSLIDBAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAATNQQGSAKNGE-----NT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 STARIWNLSENSTSGPTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:L28125; NID:g607002; PID:g607003; PIDN:AAA85775.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
16.9%; Score 462; DB 2; Length 13
Best Local Similarity 27.3%; Pred. No. 3.4e-25;
Matches 121; Conservative 74; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T18521
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1356 <8AU>
                                                                       : | ::: | ::: | ::: | :: | 1153 NSVRSVAFSSDGLILASGSDDETIKLWDVK 1482
                                          484 GGIFEVCWNAAGDKVGASASDGSVCVLDLR
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820 ISTISVVEAEWNACTQT-
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A,Gene: het-el
A;Introns: 761/3
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WD-220 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

C,Species: Nostoc sp. PCC 7120

C,Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C,Accession: AC2239

E,Raneko, T.; Nakamura, V.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B

DNA Res. 8, 205-213, 2001

A,Atitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A,Reference number: AB1807; WUID:21595285; PMID:11759840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1526 <KUR>
A;Residues: 1-1526 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75165.1; PID:g17132599; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3466
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                                                                                                                                                                                                                                                                                                                                                                    ---VHSYRGIGGIFEVC 490
                                                                                                                                                                                                                                                                                                                                                                                                          454 GOKYÁVAFMDGOVNVYDLKKINSKSRSLYGNRDGILNPLPIPLYASYQSSQDNDYÍFDLS 513
                            TSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDK 200
                                                                                                                 ----HSAP---ALDVDWQSNNTFASCSTDMCIHV 333
                                                                                                                                          284 VIILMNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFV 343
                                                                                                                                                                                                 334 CKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKE 393
                                                                                                                                                                                                                            344 YQITEKTPTGKLIGHHGPISVLEFNDTNKLLLSASDDGTLRIWHGGNGNSFYGHSQS 403
                                                                                                                                                                                                                                                                                    394 IYTIKWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPD 453
                                                                                                                                                                                                                                                                                                                       404 IVSASWV------GDDRVISCSMDGSVRLWSLKQNTLLALSIVDGVPIFAGRISQD 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 NGAHTIANNHTDMMEVDGDVEIPSNKAV-VLRGHESEVFICAMNPVSDLLVSGSGDSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IWNLSENSTSGPTQLVLRHC--IREGGODVPSNKDVTSLDWNSEGTLLATGSYDGFARIW
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                                                         TCLAMSHDGNSIVTGVENGELRIMNKTCALLNVINFHRAPIVSVKWNKDGTHIISMDVEN
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llarity 30.3%; Pred. No. 1.7e-26;
Conservative 77; Mismatches 149; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454 GRYLASGSFDKCVHIW----NTQTGAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNAAGDKVGA--SASDGSVCVL 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              514 WNCAGNKISVAYSLQEGSVVAI 535
                                                                                                                      TTIIWDAHTGEAKQQFPF-----
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Matches 118; Conserv
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ABIBION
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C)Species: Nostoc sp. PCC 7120
C)Species: Nostoc sp. PCC 7120
C)Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C)Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C)Accession: ABIBIO
C)Accession: ABIBIO
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res: 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak
A;Reference number: ABIBIO
A;Status: Preliminary
A;Residues: 1-1227 <KUR>
                                                                                                                                                                                                                                                                                             441 TLIGHDNEVNKVNFSPDGKTLASASRDNTVKLMNVSDGKFKKTLKGHTDEVFWVSFSPDG 1500
                                                                                                                                                                                                   362 NLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFD 421
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A;Cross-references: GB:BA000019; PIDN:BAB77553.1; PID:g17135007; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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            244 SYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQ 302
                                                                                                                                                                                                                                   939 -GHQG-----RIRSVAFHPDGKILASGSADNTIKLWDISDTWHSKYIRTLTGHTWWWTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             888 ITGNSLNILRGYTRDVYSVAFSPDSOILASGRDDYTIGLWNLKTGEC------HPLR
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16.0%; Score 437; DB 2; Length 12;
Best Local Similarity 31.7%; Pred. No. 1.9e-23;
Matches 102; Conservative 61; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       1612 HOAGVMSAIFSPDGKTLISGSLD 1634
                                                                                                                                                                                                                                                                                                                                                                                            482 GTGGIFEVCWNAAGDKVGASASD 504
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:2159285; PMID:11759840
A;Reference number: AB1807; MUD:2159285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1288 «KUR»
A;Cross.references: GB:BA000019; PIDN:BAB74499.1; PID:g17131893; GSPDB:GN00179
A;Experimental source: strain PCC 7120
A;Genetics:
A;Genetics:
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                1019
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WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
S.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AF2071
C;Accession: AF2071
C;Accession: AF2071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 NKDVTSLDW-----NSEGTLLATGSYDGFARIWT-KDGNLASTLGQHKGPIFALKWNKK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-1683 «KUR»
A;Cross-references: GB:BA00019; PIDN:BAB73823.1; PID:g17131215; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a112124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLG
                                                                                                                                                                                                                                                                                                                                                                                          ----TDWVYAVVFHPQGKIIATGSADCTVKLWNISTGQCLKTLSEHSDKILGMAWSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 KWSPIGPGINNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYL
                                                                                                                                                                                                                                                                                                                                                              165 LRGHESEVFICAMNPVSDLLVSGSGDSTARIMNLSENSTSGPTQLVLRHCIREGGQDVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ODRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKBIYTI
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                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                 177;
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                                                                                                                                                                                                                                                                         Length 1258;
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                                                                                                                                                                                                                                                                    ; Score 459.5; DB 2;
; Pred. No. 4.6e-25;
44; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 451; DB 2; L. Pred. No. 2.9e-24; L. Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1074 GOLLASASADOSVRLWD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1290 SSDGKAIASASRDNTIKLWNRHGIELE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGSQDQTVRIWNVKTGECLQILR 1227
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                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.5%;
Matches 102; Conservative 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.5%;
28.5%;
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Best Local Similarity 28.5%
Matches 109; Conservative
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41;

Length 1708;

350

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EVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPN 410
                                                                                                                                                                                                                                                                   1461 LWH-QDGKILHTLQGHQDAVLAVAWSSDSQVIASAGKDKIVKIWSQG-GQLLHTLQGHTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 ANIMIASASFDSTVRIMDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWN
                                                                                                                                   119 NQQGSAKNGENTANGEENGAHTIA---NNHT-DMMEVDGDVEIPSNKAVV---LRGHESE
                                                                                                                                                                                  1298 NRQG---NLLKTLSGHTAGVTAVTFSPNGETIGSASIDATLKLWSPQGLLLGTLKGHNSW
                                                                                                                                                                                                                                    172 VFICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSL
                                                                                                                                                                                                                                                                                                                                     232 DWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                   IWDAHTGEAKQQFPFHSAPALDVDWQSNN-TFASCSTDMCIHVCKLGQDRPIKTFQGHTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1627 -QKGTLLMVLKGDKDELTSVTFSPDSQILAVGGGNGKVIFLNL 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 TOTGALVHSYRG-TGGIFEVCWNAAGDKVGASASDGSVCVLDL 512
                                  Query Match
16.0%; Score 436.5; DB 2;
Best Local Similarity 30.5%; Pred. No. 3.3e-23;
Matches 123; Conservative 70; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.9%
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary
A,Molecule type: DNA
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A;Gene: all0284
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C.Species Nostoc sp. PCC 7120
A.Note: Nostoc sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C.Accession: AEI866
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A.Itle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                   R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Astitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: A14493
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A;Cross-references: GB:BA00020; PIDN:BAB78213.1; PID:g17135667; GSPDB:GN00180
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 LASTLGOHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQOFPFHSAPALDV--D 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 GHESEVFICAWNPVSDLLVSGSGDSTARIWNLSE----NSTSGPTQLVLRHCIREGGQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- DVPSNK------DVTSLDWNSEGTLLATGSYDGFARIW-TKDGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WQSNNTFASCSTDMCIHVCKLG------QDRPIKTFQGHTNEVNAIKWDPTGNLLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 CSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDSTVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSADRTIKLWSPHTGQCLHTLHGHGSWVWAIAFSLD------DKLLASGSYDHTVKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.0%; Score 436.5; DB 28.7%; Pred. No. 2e-23;
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Best Local Similarity 28.74
Matches 108; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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A;Genome: plasmid
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C;Accession: AD1842
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Residues: 1-1711 <KUR>
A, Cross-references: GB: BA000019, PIDN: BAB77808.1, PID:g17135262, GSPDB:GN00179
A, Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKAVVLRGHESEVFICAWNPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.2%; Score 415; DB 2; Length 1711; 24.9%; Pred. No. 1.2e-21; ive 75; Mismatches 180; Indels 110
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| SASDDGTIRLWSLDGRPLITI--------
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A, Status: preliminary A, Molecule type: DNA A, Residues: 1-1708 < KUR> A, Cross-references: GB:BA000019; PIDN:BAB72436.1; PID:g17129823; GSPDB:GN00179 A, Experimental source: strain PCC 7120

A;Gene: all0478

Genetics

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WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

G;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

G;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

G;Accession: AG1889

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IWSLDGKKQL----VVLREEKGEGFNSVAF 376
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A,Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 SEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 AHTGEAKQQFPFHSAPALDVDWQ----SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
14.8%; Score 403.5; DB 2; Length 934;
Best Local Similarity 23.1%; Pred. No. 3.5e-21;
Matches 128; Conservative 115; Mismatches 197; Indels 113;
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WD repeat protein - fission yeast (Schizosaccharomyces pombe)
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A;Molecule type: DNA
A;Residues: 1-934 <KUI
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A,Gene: all0664
                                      1659
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AC1842
WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. Strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AC1842
C;Accession: AC1842
R;Kaneko, T: Nakamura, Y: Wolk, C.P.; Kuritz, T.; Sasamoto, S: Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, G
DNA Res 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Recession: AC1842
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-1747 ~kUR>
A;Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179
C;Genetics:
A;Gene: all0283
                                                                                                                                                                                                                 1488 QILASGSADKTIKLMSV-NGRLIKTLIGHNGWVTDIKFSADGKNIVSASADKTIKINSL- 1545
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                                                                                                                                                                           320 NTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMK
                                                                                                                                                                                                                                                                                                                                                                                                                      440 KHOEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYRG-TGGIFEVCWNAAGDKV
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N;Alternate names: protein sll0163
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
C;Accession: S76086
S;Xotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                     ;Status: preliminary; translated from GB/EMBL/DDBJ;Molecule type: DNA;Rolecule type: DNA;Rosidues: 1-564 <WOO>;Ecoss-references: EMBL:AL031764; PIDN:CAA21113.1; GSPDB:GN00068; SPDB:SPCC1235.09;Experimental source: strain 972h-; cosmid c1235;Genetics:
                                                                                                                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 NGFCEHNNSNDHQLKILQDKGSGSPSSPVMPFKDKIEKRDIDITWADESNVEKDPARPIA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 NNHTDMMEVDGDVEIPSNKAVVLRGHE---SEVF-----ICA-WNPVSD----LLV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 TGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGBAK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40883
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: 221954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 YAFFSGVIEİYDSHGSQILSFHNNKGPVLSİKMSGTDTYLAAGSADGTITLFD----QLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPTGNLLASCSDDMTLKIWSMKQD---NCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLM
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                                                                                                                                                                                                                                                                                                                                                                                                                         60 VEAEV-----SINEDG--TLFDGRPIESLSLID------AVMPDVVQT-----
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                                                                                                                                                                                                                                                                                                                        Length 564;
                                                                                                                                                                                                                                                                                                                    Query Match
14.3%; Score 391.5; DB 2;
Best Local Similarity 24.7%; Pred. No. 1.3e-20;
Matches 134; Conservative 106; Mismatches 201;
                                                                                                                                                                                                                                                                    A,Map position: 3
A;Introns: 18/1; 273/3; 413/3
                                                                                                                                                                                                                                              Gene: SPDB:SPCC1235.09; Map position: 3
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Ay2195

hypothetical protein alr3119 [imported] - Nostoc sp. (strain PCC 7120)

hypothetical protein alr3119 [imported] - Nostoc sp. (strain PCC 7120)

A;Species Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision-14-Dec-2001 #text_change 09-Dec-2002

C;Date: 14-Dec-2001 #sequence_revision-14-Dec-2001 #text_change 09-Dec-2002

B;Raneko, T: Nakamura, Y: Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. D, Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A; Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g1001396; PIDN:BAA10064.1; PID:d1010715
to the EMBL Data Library, June 1996
WD repeat homology
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A,Molecule type: DNA
Residues: 1-676 «KUR»
A,Cross-references: GB:BAC00019; PIDN:BAB74818.1; PID:g17132214; GSPDB:GN00179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --RPLLTLAGHQSIVYQARFSPEGNLIATVSADHTARLWD-RSGKTVAVLYGHQGLVGTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 RDKLAQQHAAAAAAAATNQQGSAKNGENTANGE--ENGAHTIANNHTDMMEVDGDVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDKTARLWTTEGECVAVLADHOGWVREGOFSPDGOWIVTGS----ADKTAQLWNVLG----
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                                                                                                                                                                                                                                                                        translation not shown
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A, Title: Sequence analysis of the genome of the unicellular
                                                                                                                                    A;Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
14.3%; Score 390.5; DB 2;
Best Local Similarity 28.5%; Pred. No. 7.2e-20;
Matches 107; Conservative 53; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMEL:05399; GB:AB001339; A; Cross-references: EMEL:05399; GB:AB001339; A; Cross-references: EMEL:05399; GB:AB001339; A; Note: the nucleotide sequence was submitted b; Superfamily: unassigned WD repeat proteins; F;1051-1084/Domain: WD repeat homology wWD01>F;1031-1166/Domain: WD repeat homology wWD03>F;1131-1166/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD repeat homology wWD03>F;1174-1207/Domain: WD03-F;1174-1207/Domain:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <WD10>
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                                                                                                                                                                                                          A;Accession: S76086
A;Status: nucleic acid sequence not shown;
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F,1297-1330/Domain:
F,1338-1371/Domain:
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completed: August
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A;Cross-references: GB:BA00019; PIDN:BAB76533.1; PID:g17133971; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                          14.1%; Score 385.5; DB 2; Length 676; 24.2%; Pred. No. 4.6e-20; ive 82; Mismatches 191; Indels 125;
                                                                                                                                                                                                                     21 FSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYVEA-------
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C;Genetics:
A;Gene: alr3119
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Matches 120; Conservative
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                         1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV 60
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            MSISSDEVNFLVYRYLOESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
NCBI_TaxID=10090;
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SMART; SMO0320; WD40; 8.
PROSITE; PS50896; LISH; 1.
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BMBL: AK036064; BAC29294.1; -.
PIR; PT0651; PT0651.
MGD; MGI:2441730; Iral.
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                                                                                                                                                                                                                                                                                                                                                                                       181 SDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGODVPSNKDVTSLDWNSEGTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTIIWDAHTGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSY
                                                                                                                                                                              1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                   Gaps
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Wararyota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                   ·.
                                                                                        Length 514;
                                                                                                                                   Indels
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
SEQUENCE 514 AA; $5661 MW; 13BEC1C2C7F8BF14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                      99.9%; Score 2727; DB 11;
99.8%; Pred. No. 3.2e-184;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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Interpro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
                                                                                             Query Match
Best Local Similarity 99.8
Matches 513; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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IRA1 OR 8030499H02RIK.
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SEQUENCE FROM N.A.
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DB 13; Length 519;
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STRAIN=CS7BL/6; TISSUE=Brain;
MEDLINE=2238257; PubMed=12477932;
Strausberg R.L., Faingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler
                                                                                                                                              Indels
                                                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 519
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Last annotation update)
                                                                                                Score 2645.5; DB 13
Pred. No. 1.9e-178;
2; Mismatches 12;
                                                       5E998EDC8C892296
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                                                       56043 MW;
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                                                                                                   96.9%;
96.3%;
         EMBL; AY225088; AAP20646.1;
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                                                                                                Query Match
Best Local Similarity 96.3
Matches 500; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                       AA;
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01-OCT-2003 (
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                                                                                                                                                                                                                                                                               Gaps
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"Tusion Protein of Retinoic Acid Receptor (alpha) with Promyelocytic
Leukemia Protein or Promyelocytic Leukemia Zinc Finger Protein
Recruits N-CoR-TBLRI Corepressor Complex to Repress Transcription in
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Nuclear receptor co-repressor complex subunit TBLR1.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                      Length 514;
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PRINTS; PR00320; GPROTEINBRPT.

ProDom; PD00018; WD40; 3.

SMART; SM0067; LisH; 1.

SMART; SM00320; WD40; 8.

PROSITE; PS50896; LISH; 1.

PROSITE; PS50082; WD_REPEATS 1; 4.

PROSITE; PS50294; WD_REPEATS_2; 6.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

SEQUENCE 514 AA; 55689 MW; 13BED3753A725029, CRC64;
                                                                                                                                                                                                                                 Score 2724; DB 11;
Pred. No. 5.3e-184;
1; Mismatches 1;
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                                                                                                                                                                                                                                 99.78;
                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6
Matches 512; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xen
NCBI_TaxID=8355;
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STRAIN=CS/BL/60; TISSUE=Hypothalamus;
MEDLINE=2235463; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
malyais of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:555-573 (2002).
FINE; PT0651; PT0651.
FINE; PT0651; PT0651.
MGJ; MGT:1336172; PLIX.
InterPro; IPR006594; LisH.
InterPro; IPR006694; LisH.
FEAM; PF00400; W440; R.
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420 SNPNSNIMLASASFDSTVRLWDVERGVCIHTLITKHQEPVYSVAFSPDGKYLASGSFDKCV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Prodom; PD000018; WD40; /3.

SMART; SM00667; LisH; 1.

PROSITE; PS50896; LISH; 1.

PROSITE; PS5080678; WD REPEATS 1; 4.

PROSITE; PS500878; WD REPEATS 2; 6.

PROSITE; PS500874; WD REPEATS 2; 6.

PROSITE; PS500874; WD REPEATS 2; 6.

PROSITE; PS500874; WD REPEATS REGION; 1.
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90.2%; Score 2462.5; DB 11
Best Local Similarity 87.5%; Pred. No. 1.6e-165;
Matches 462; Conservative 27; Mismatches 24;
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01-OCT-2003 (TrEMBLrel. 25, Last ann
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   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Rab Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Rab Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rabieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
R. Achards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
R. Palekon B., Ketreman M., Madan A.M., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rabieto R.M., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
T. "Generation and initial malysis of more than 15,000 full-length human
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Straubberg R.;
Stubmitted (1AN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (1AN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK038674: BAC30092.1;
PRIR; PF06651; PF0651.
PRIR; PF06651; PF06651.
InterPro; IPR006594; Lish.
InterPro; IPR006594; Lish.
InterPro; IPR00400; Wa40; B.
PRINTS; PR00320; GPROTEINBRPT
PRODom; PD000018; W040; 3.
EMART; SM00567; Lish; 1.
SMART; SM00520; WD40; 8.
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PROSITE; PS00678; WD REPEATS 1; 4.
PROSITE; PS50082; WD REPEATS 2; 6.
PROSITE; PS50094; WD REPEATS REGION; 1.
SEQUENCE 527 AA; 56802 MW; 146435A9C51DFDA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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STRAIN=C57BL/6; TISSUE=Brain;
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XX MEDLINE—2238825; PubMed=12477932;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XA Diatchench E., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

XA Scarse M.B., Bonard M.F., Casavant T.L., Scheetz T.E.,

XA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XA Sask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XA Villalon D.K., Muxny D.M., Sodergrar B.J., Lu X., Glubs R.A.,

XA Villalon D.K., Muxny D.M., Sodergrar B.J., Lu X., Glubs R.A.,

XA Hathing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

XA Reseley R.W., Touchman J.W., Green B.D., Dickson M.C.,

XA Ricking M., Matan J., Schmutz J., Myers R.M., Butterfield Y.S.,

Xrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

XH Generation and initial analysis of more than 15,000 full-length human

XI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2022).
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                                                    360 GHTNEVNAIKWDPSGMLLASCSDDMTLKINSMKQDACVHDLQAHSKEIYTIKWSPTGPAT
                                                                                                                                                      SIND SNIMLASAS FDSTVRLWDVERGVCIHTLIKHQEPVYSVAFSPDGKYLASGSFDKCV
                      GHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGT
                                                                                                                       407 NNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDKCV
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86.0%; Pred. No. 8.2e-164;
iive 33; Mismatches 27; Indels 14
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC052304; AAH52304.1; -.
RINGERPO; IPR006594; Lish.
RINGERPO; IPR001680; WD40.
R FRIM: PR00400; MD40; 8.
R PRINTS; PR00320; GRROTBINBRPT.
R SWART; SM00320; WD40; 3.
R SWART; SM00320; WD40; 3.
R PROSITE; PS50896; LISH; 1.
R PROSITE; PS5082; WD REPEATS 1; 4.
R PROSITE; PS5082; WD REPEATS 1; 4.
R PROSITE; PS5082; WD REPEATS 2; 6.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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Matches 453; Conserv
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52 MSITSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGTLVPPAALISILQKGLQYV
                                                                                                                                                471 NPNSNIMLASASFDSTVRLWDIERGVCTHTLTKHQEPVYSVAFSPDGKYLASGSFDKCVH
                                                                                                                                                                                                    HESEVFICAMNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKD
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                                                     EAEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAT-
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Prodom; PRO0018; W040; 3.
SMART; SM00320; WD40; 3.
PROSITE; PS00678; WD REPEATS_1; 4.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD REPEATS_REGION; 1.
NON TER 1 1 SEQÜENCE 412 AA; 44356 MW: RR7A010EANA
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PIR; PT0551; PT0651.
MGD; MGI:1336172; Tbllx.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 8.
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MEDINE-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Hichards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Burton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
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A brill J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A brill J.E., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
A ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
A ballew R.M., Basu A., Baxendale J., Brotakter P.,
A burtis K.C., Busam D.A., Burler H., Cadieu E., Center A., Chandra I.,
A burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Fleischmann W.,
A podson K., Doug L.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P.,
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Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
A lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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                                                                                     9
                                                                                                                                                                                           121 PSNKDVTSLDMNSDGTLLATGSYDGFARIWTEDGNLASTLGQHKGPIPALKWNKKGNYIL
                                                                                                                                                                                                                                                    241 KTFQGHTNEVNAIKWDPSGMLAASCSDDMTLKIWSMKQDACVHDLQAHSKEIYTIKWSPT
                                                                                                                                                                                                                                                                                                                                                    403 GPGTNNPNANLMLASASFDSTVRLMDVDRGICIHTLTKAQEPVYSVAFSPDGRYLASGSF
                                                                                                                                                                                                                                                                                                                                                                   108 AAAAAAAAATN-----QQGSAKNGENTANGEENGAHTIANNHTDMMEVDGDVEIPSNKA
                                                                                                                                              61 TVLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLNENSNGGSTQLVLRHCIREGGHDV
                                                                                                                                                                           PSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFIL
                                                                                   2 AAATATSTAATTPAAAAQQNPPKNGEATVNGEENGAHAI-NNHSKPMEIDGDVEIPPSKA
                                                                                                                   163 VVLRGHESEVFICAMNPVSDLLVSGSGDSTARIMNLSENSTSGPTQLVLRHCIREGGQDV
                                                                                                                                                                                                                                                                                            KTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKBIYTIKWSPT
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            361 DKCVHIMNTQSGSLVHSYRGTGGIFEVCWNARGDKVGASASDGSVCVLDLRK 412
                                                                                                                                                                                                                                                                                                                                                                                                             463 DKCVHIWNTQTGALVHSYRGTGGIFEVCWNAAGDKVGASASDGSVCVLDLRK 514
                              .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
 Length 412;
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                              26;
 DB 11;
71.6%; Score 1956; DB 11;
87.1%; Pred. No. 6.4e-130;
ative 21; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                              Matches 359; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EBI protein.
EBI OR CG4063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9XZK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden Krämos I., Simpson M., Skrupski M.P., Smith T.,
RA Spier E., Paradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA J., Yeh R.-F., Zaveri J.S., Zhan M., Zhong K., Zho Q., Zheng L.,
Zheng X.H., Myers E.W., Zhong W., Zhou X., Zhu X., Smith H.O.,
RIFE Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
R. The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDQSASEVDSSGNAANNAGGTYAGNNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calliker S.E., George R.A., Galle R.F., Hoskins R.A., Svirskas R.R., Calniker S.E., George R.A., Arcaina T.T., Baxter E., Blazej R.G., Calniker S.E., George R.A., Arcaina T.T., Baxter E., Blazej R.G., Chaver C., Chew M., Doyle C.M., Farfan D.E., Flanagan J., Chavez C., Chew M., Doyle C.M., Farfan D.E., Flanagan J., Chew M.A., Marda P., Moshrefi A.R., Moshrefi M., Nixon K., Park S., Pfeiffer B., Punch E., Snir E., Twomey B., Pacleb J.M., Park S., Pfeiffer B., Punch E., Snir E., Twomey B., Wan K.H., Zhang R., Zieran L.L., Rubin G.M.; Snir E., Twomey B., Chem K.H., Zhang R., Zieran L.L., Rubin G.M.; Snir E., Twomey B., Chem K.H., Zhang R., Zieran L.L., Rubin G.M.; Snir E., Twomey B., BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; BMBL; Acto5389; AAP51501.1; AAP51801.1; BMBL; Acto5389; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP51801801; AAP5180180
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MEDLINE-99234084; PubMed=10215623;
Dong X., Tsuda L., Zavitz K.H., Lin M., li S., Carthew R.W.,
Zipursky S.L.;
"ebi regulates epidermal growth factor receptor signaling pathways in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.8%; Score 1906.5; DB 5; Length 700; Best Local Similarity 54.8%; Pred. No. 4.2e-126; Matches 385; Conservative 49; Mismatches 77; Indels 191; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAEVSINEDGTLFDGRPIESLSLIDAVMPDV-----VQTRQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSC686; LISH; 1.
PROSITE; PSC696; LISH; 1.
PROSITE; PSC678; WD *RPPATS_1; 3.
PROSITE; PSC678; WD *RPPATS_2; 6.
PROSITE; PS56294; WD *REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0320; GPROTEINBRPT.
PRODONIS; WD40; 3.
SMART; SMO0567; LisH; 1.
SMART; SM00320; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes Dev. 13:954-965(1999).
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H.C.,

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GVEREHEGDRNRAKEKDRHEKQKEREREREKLEREKEREREKIEREKEREREKMEREIFE 180
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REKDRLKLEKEREIEREREREKIEREKSHEKQLGDADREMVIDQTDKEIAGDGSTGAEPM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 DIVMTPTSQTSHIPNSDVRILEGHTSEVCACAWSPSASLLASGSGDATARIWSIPEGSFK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 ASTLGQHKGFIFALKWNKKGNFILSAGVDKTTIIWDAHTGEAKQQFPFHSAPALDVDWQS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AEVSINEDGTLFDGRPIESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 MEANLSNSEVDIDEDFSFF--QPLDLISKDVKELQDMLREKKRKERDMEKERDRSKENDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IPSNKAVVLRGHESEVFICAWNPVSDLLVSGSGDSTARIWNLSENSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 ISTLSKHKGPIFSLKMNKKGDYLLTGSVDRTAVVWDVKABEWKQQFEFHSGPTLDVDWRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SLTSVELNFLVPRYLQESGFTHAAFTLGYEAGINKSNIDGNMVPPGALIKFVQKGLQYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GP----TQLVLRHCIREGGQDVPSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 NNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQDNCVHDLQAHNKE1YT1KWSPTGPGTNNPNANLMLASASFDSTVRLWDVDRGICIHTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYVE
Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H., Yu G., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 613;
                                                                                                                                                                                                                                            Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL; A2007645; BAB09017.1; -. EMBL; A2007698; AALIS238.1; -. EMBL; A2007698; AALIS238.1; -. EMBL; A2007698; AALIS2871.1; -. EMBL; A20076894; Lish. InterPro; IPR0016894; Lish. InterPro; IPR001680; WD40. Pfam; PF000400; WD40; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69772 MW; 04F40772311C0E76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.2%; Pred. No. 1.4e-89; ive 90; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GDVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.8%; Score 1388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSS0896; LISH; 1.
PROSITE; PS00678; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 6.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AAATNQQGSAKNGENTANGE-
                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PRO0320, GPROTEINBRPT.
ProDom, PD000018, Wb40; 2.
SWART; SM00667, LisH; 1.
SWART; SM00320, WD40; 8.
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                                                                                                                                                                                                                            "Arabidopsis ORF clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 NHTDMMEVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.2
Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
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                                                                                                                                    299 GNNVQSGSSNAQSSAPSGTISSSTSGGAGTPAALVPMDIDENIEIPESKARVLRGHESEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 WDASTGQCTQQFAFHSAPALDVDWQTNQAFASCSTDQRIHVCRLGVNEPIKTFKGHTNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGNQASTGGSNSTSTPAGGDLAAPGASQKKSQNSNEAGSSSSGNAGNANATSTDDAASS
                                                                                                                                                                                                                                                                                                  FICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                               FICAWNPSRDLLASGSGDSTARIWDMSDANTNS-NQLVLRHCIQKGGAEVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII
                                                                                                                                                                                                                                                                                                                                                                                                                                              WNCDGSLLATGSYDGYARIWKTDGRLASTLGQHKGPIFALKWNKCGNYILSAGVDKTTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNAN
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                                                                                                                                                                                                     -----MEVDGDVEIPSNKAVVLRGHESEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 WDAHIGBAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear Cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicoryledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98162728; PubMed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TREMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Genomic DNA, chromosome 5, TAC clone:K8K14 (ATSg67320/K8K14_4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGQLVHSYKGTGGIFEVCWNSKGTKVGASASDGSVFVLDLRK 699
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A
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61

Gaps

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Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                              PRINTS; PR00320; GPRCTEINBRPT.
PRODON; PD000018; WD40; 1.
SMART; SM00667; LisH; 1.
SMART; SM00320; WD40; 3.
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 40.3%;
Matches 217; Conservative
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PROSITE; PS00037; MYB_1; 1
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Podospora anserina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidaa; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 201;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018512; AAH18512.1;
InterPro.; IPRO1860; WJ40.
PRINTS; PRO0400; WJ40. 4.
PRINTS; PRO0400; WJ40. 4.
PRINTS; PRO0400; WJ40; 4.
PRODM; PD000019; WJ40; 2.
PROSITE; PS00678; WD REPEATS 1; 2.
PROSITE; PS00678; WD REPEATS 2; 3.
PROSITE; PS00679; WD REPEATS 2; 3.
PROSITE; PS00929; WD REPEATS 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                 Ol-WAR-2002 (TrEMBLrel. 20, Created)
Ol-WAR-2002 (TrEMBLrel. 20, Last sequence update)
Ol-War-2003 (TrEMBLrel. 23, Last annotation update)
Similar to IRAl protein (Fragment)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
40.3%; Score 1101; DB 11;
Best Local Similarity 99.5%; Pred. No. 5.4e-70;
Matches 200; Conservative 0; Mismatches 1;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                    PRT;
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     612
     598 AACFADNSVCVLDFR
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EBI OR CG4063.
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                                                                                    Q8VEG3
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095RJ9
                                                     RESULT 11
                                                                      Q8VEG3
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61 EVEWSVGEDGEV--ARPIEGLSLIDAVMPEVKPLKPIVKTEPGKPGAVDSSAPAGGNQNN 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 NAKPEIKIEPGTGVAGSAGGNKIAGSTTGTSTPTDQSASEVDSSGNAANNAGGTYAGNNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGNQASTGGSNSTSTPAGGDLAAPGASQKKSQNSNEAGSSSSGNAGNANATSTDDAASS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 TSTNGNSSTSSSVEQPTSGLTPAGGTVSTSNPDAAASGGASTATGSKAPSGAVTIRVGAQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------MEVDGDVEIPSNKAVVLRGHESEV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FICAMNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 WNSEGTLLATGSYDGFARIWTKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTII 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MSFSSDEVNFLVYRYLQESGFLHSAYVFGIESHISQSNINGALVFFAALLTILQKGLLYT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WDAHTGEAKQOFPHSAPALDVDWQSNNTFASC------STDMCIHV-CK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDASTG-----PMHPAICL----SQCSSLGCGLADKPGLCLLQYGSADTCVPVGCK 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSISSDEVNFLVYRYLQESGFSHSAFTFGIESHISQSNINGALVPPAALISIIQKGLQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.7%; Score 920.5; DB 5; Length 524; 40.3%; Pred. No. 1.2e-56; Indels 217; ive 37; Mismatches 67; Indels 217;
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S
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                           Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY061326; AAL28874.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROGITE; PS00678; WD_REPEATS_1; 2.
PROSITE; PS50082; WD_REPEATS_2; 3.
PROSITE; PS50284; WD_REPEATS_2; 3.
REPORTE; WD_rEPEATS_REGION; 1.
SEQUENCE 524 AA; 52529 MW; GC3D86110BA18D65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 ANGEE------
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U-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CM-2003 (TrEMBLrel. 25, Last annotation update)
Beta transducin-like protein HET-E2C*4.
                                                                                                                           FlyBase; FBgn002344; ebi.
GO; GO:000074; P:regulation of cell cycle; IMP.
InterPro; IPR006594; LisH.
InterPro; IPR001005; Myb DNA_binding.
InterPro; IPR001660; Wb40.
Pfam; PF00400; WD40; 3.
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Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 27.9%
hes 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Podospora anserina
                     NCBI TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1149
                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1149 -----RVASGSIDGTIKIWDAASGTCTQTLEGHGGWVHSVAFSPDGQRVASGSIDG 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 ANGEENGAHTIANNHTDMMEV----DGD-VEIPSNKAVV------LRGHESEV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTNNPNANLMLASASFDSTVRLWDVDRGICIHTLTKHQEPVYSVAFSPDGRYLASGSFDK 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTI 291
                                                                                                                                                                                                                                                                                                                                                                                                                             78 IESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAATNQQGSAKNGE-----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              871 ASG--TGTQTLEGHGGSVWSVAFSPDGQRVASGSDDKTIKIWDAASGTCTQTLEGHGSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 FICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 IWDAHTGEAKQQFPFHSAPALDVDWQSNNTF-----ASCSTDMCIHVCKLGQDRPIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1035 IWDTASGTCTQTLEGHGG-----WVQSVAFSPDGQRVASGSNDHTIKIWDAASGTCTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 FQGHTNEVNAIKWDPTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        820 ISTISVVEAEWNACTQT-----LEGHGSSVLSVAFSPDGQRVASGSDDKTIKIWDT
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                       Espagne E. M. Balhadere P., Begueret J., Turcq B.;
"A new family of WD40 proteins implicated in vegetative incompatibility; evidence for a major role of WD40 repeat domain in the specificity of het-e and het-d genes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF323583, AAL37299.1;
InterPro; IPR00111; NACHT_WTPase.
                                                                                                                                                                                                                                                                                                                                                                                               74;
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 480; DB 3; Length 1356; 27.8%; Pred. No. 5.5e-25; ive 78; Mismatches 186; Indels 74
                                                                                                                                                                                      Pram; Pro6729; MACHT; 1.
Pram; Pro6729; MACHT; 1.
Pram; Pro6729; MACHT; 1.
Pram; Pro6729; MACHT; 1.
PRINTS; PR00320; MACHT; 1.
ProDom; PR0811E; PS5081; MACHT; 1.
PROSITE; PS5082; MD REPEATS 1; 10.
PROSITE; PS5024; WD REPEATS 2; 10.
PROSITE; PS5024; WD REPEATS 2; 10.
PROSITE; PS5024; MD REPEATS 1.
Repeat; WD repeat; MD REPEATS 1.
Repeat; WD repeat 3356 AA; 149702 MW; 33148AF4A7B82826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVHIWNTQTGALVHSYRGTGG-IFEVCWNAAGDKVGASASDGSVCVLD
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Best Local Similarity
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                                                              SEQUENCE FROM N.A.
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08X1PS
10 08X1P
AC 08X1P
DT 01-MA
DT 01-MA
DT 01-MA
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1035 IWDTASGTCTQTLEGHGGWVWSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEGHGD 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWDAHTGEAKQOFPFHSAPALDVDWQ-SNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTN 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 EVNAIKWDFTGNLLASCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPN 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 WNSEGTLLATGSYDGFARIW-TKDGNLASTLGQHKGPIFALKWNKKGNFILSAGVDKTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 ANGEENGAHTIANNHTDMMEV----DGD-VEIPSNKAVV-------LRGHESEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                871 ASG--TGTQTLEGHGGSVWSVAFSPDGQRVASGSDDKTIKIWDAASGTCTQTLEGHGSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 FICAWNPVSDLLVSGSGDSTARIWNLSENSTSGPTQLVLRHCIREGGQDVPSNKDVTSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IESLSLIDAVMPDVVQTRQQAYRDKLAQQHAAAAAAAAAATNQQGSAKNGE-----NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62;
Espagne E., Balhadere P., Begueret J., Turcq B.;
Espagne E., Balhadere P., Begueret J., Turcq B.;
I ncompatibility evidence for a major role of WD40 repeat dome incompatibility; evidence for a major role of WD40 repeat dome incompatibility of het-e and het-d genes.".

I the specificity of het-e and het-d genes.".

EMBL, AF223582; AAL37288.1; -.

EMBL, AF223582; AAL37288.1; -.

InterPro; IPR001611; NACHT_NTPase.

InterPro; IPR001681; WD40.

Pfam; PF00400; WD40; 10.

PRODOM; PRO0320; GPROTEINBRPT.

PRODOM; PRO0018; WD40; 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.5%; Score 477; DB 3; Length 13:
27.9%; Pred. No. 9e-25;
ive 78; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1356 AA; 149720 MW; 9A80777304B361D0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00320; WD40; 10.
PROSITE; PS50837; NACHT; 1.
PROSITE; PS50837; NACHT; 1; 10.
PROSITE; PS5082; WD_REPEATS_1; 10.
PROSITE; PS50824; WD_REPEATS_2; 10.
Repeat; WD_repeat.
SEQUENCE 1356 AA; 149720 MW; 9A80777
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Q8X1P3
DD Q8X1P
AC Q8X1P
DT O1-MA
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DT O1-MA
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Best Local Similarity 27.7%; Pred. No. 2e-24;
Matches 128; Conservative 78; Mismatches 194; Indels
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SEQUENCE FROM N.A.
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